Sequence:

Run on:

Searched:

Database

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| C9912_6| prodata 2/2 pina/US101A_COMB. seq: |
| C9912_6| prodata 2/2 pina/US101B_COMB. seq: |
| C9912_6| prodata 2/2 pina/US
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02:
04:
05:
March 11, 2004, 20:36:42; Search time 2283.3 Seconds (without alignments) 1386.917 Million cell updates/sec
                                                                                                                                                                                                                                                                                                             90
                                                                                                                                                                                                                                                                                                             1 atgagagtgaaggagaaata......tgttgatgatctgtagtgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: /cgn2_6/ptodata/2/pna/PcTUS_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/BcTUS_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
12: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
15: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
16: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
17: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/USO9_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/USO9_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/USO9_COMB.seq:*
23: /cgn2_6/ptodata/2/pna/USO9_COMB.seq:*
24: /cgn2_6/ptodata/2/pna/USO9_COMB.seq:*
25: /cgn2_6/ptodata/2/pna/USO9_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/USO9_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/USO9_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/USO9_COMB.seq:*
29: /cgn2_6/ptodata/2/pna/USO9_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/USO9_COMB.s
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                  37577330 segs, 17593059518 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                  nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                          IDENTITY NUC Gapont 1.0
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Maximum DB seg length: 2000000000
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                                                                                                                                                                                                                                                                                       Perfect score:
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                                                                                                                     ,
                                                                                                                  OM nucleic
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

9 09

Gape

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Length 90;

us-10-003-035-74.rnpm

Score

Result No.

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RESULT 3

US-10-280-915-74

US-10-280-915-74

Sequence 74, Application US/10280915

GENERAL INFORMATION:

APPLICANT: Wang, Danher

TITLE OF INVENTION: MULTIVALENT VACCINATION USING RECOMBINANT ADENOVIRUS

TITLE OF INVENTION: MUMBER: US/10/280,915

CURRENT FILING DATE: 2002-10-24

PRIOR APPLICATION NUMBER: US 09/585,599

PRIOR PILING DATE: 2000-06-02

PRIOR FILING DATE: 2001-06-04

PRIOR PELING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-10-01

WUMBER OF SEQ ID NOS: 75

SOFTWARE: PATENTION NUMBER: US 10/003,035

WUMBER OF SEQ ID NOS: 75

SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Danher
APPLICANT: Wang, Danher
TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
FILE REFERENCE: 22488-712
CURRENT APPLICATION NUMBER: US/10/003,035
CURRENT FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-04
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.1
ENGTH: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGAGAGTGAAGGAAAATATCAGCACTTGTGGAGATGGGGGGTGGAGATGGGGGCACCATG
                                                                                                                                                                                                          1 ATGAGAGTGAAGGAGAATATCAGCACTTGTGGAGATGGGGGTGGGAGATGGGGCACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 90; DB 43; Length 90; 100.0%; Pred. No. 7.7e-18; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: DNA encoding gp120 signal peptide
                    FEATURE: OTHER INFORMATION: DNA encoding gpl20 signal peptide pcr-us02-35112-74
                                                                                                      ; DB 1; L
; 7.7e-18;
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                                                                                                                                             0; Mismatches
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100.0%; Pred. No.
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US-10-03-035-74
Sequence 74, Application US/10003035
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial sequence
TYPE: DNA
ORGANISM: Artificial sequence
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Matches 90; Conservative
                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 90; Conservative
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; Sequence 74, Application PC/TUS0235112
; GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
FILE REPERENCE: 22488-740
CURRENT APPLICATION NUMBER: PCT/US02/35112
CURRENT FILING DATE: 2002-11-01
PRIOR FILING DATE: 2000-06-02
PRIOR PILING DATE: 2001-06-02
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-01
NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 74
LENGTH: 90
                                                                                                                                                                                                                                                       Sequence 66, Appl
Sequence 42, Appl
Sequence 42, Appl
Sequence 42, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 135, Appl
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Sequence 141, App
Sequence 32, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                           Sequence 74, Appl
Sequence 58, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
                                                                                                                      Sequence 74
                                               Description
                                                                                   PCT-USCD-35112-74
US-10-286-335-74
US-10-286-332A-74
US-10-286-332A-74
US-10-286-332A-74
US-10-286-332A-11
US-10-286-332A-11
US-10-286-332A-11
US-10-286-332A-11
US-10-286-332A-12
US-10-286-332A-14
US-10-286-332A-14
US-10-286-332A-14
US-10-286-332A-14
US-10-286-332A-14
US-10-286-332A-18
US-10-286-332A-18
US-10-286-332A-18
US-10-286-332A-18
US-10-286-332A-35
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PCT-US91-08843A-1
PCT-US91-08843A-1
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US-08-417-210-141
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US-08-458-964A-1
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Match Length
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Gaps

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MOLECULE TYPE:
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Best Local S
Matches 90
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                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Danher:
TITLE OF INVENTION: METHOD OF VACCINATION THROUGH SEROTYPE ROTATION
FILE REFERENCE: 22488-738
CURRENT APPLICATION NUMBER: US/10/286,332A
CURRENT APPLICATION NUMBER: US 99/585,599
PRIOR APPLICATION NUMBER: DOT-03-17
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: DOT-06-04
PRIOR APPLICATION NUMBER: US 10/003,035
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 74
LENGTH: 90
                                                                                                                                                                                               1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGGCACCATG
                                                                                                                                                                                                                                1 AIGAGAGTGAAGGAGAAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG
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                                                                                                                           Length 90;
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GENERAL INFORMATION:
APPLICANT: Shiver, John W
APPLICANT: Liu, Margaret A
APPLICANT: Lerry, Helen C
TITLE OF INVENTION: COORDINATE IN VIVO GENE EXPRESSION
NUMBER OF SEQUENCES: 100
                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: DNA encoding gp120 signal peptide
US-10-286-332A-74
                                                                    ; OTHER INFORMATION; DNA encoding gp120 signal peptide US-10-280-915-74
                                                                                                                       100.0%; Score 90; DB 48;
100.0%; Pred. No. 7.7e-18;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue, P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
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United States of America
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LENGTH: 90
TYPE: DNA
ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 90; Conservative
                                                                                                                                                                    90; Conservative
                                                                                                                                                Best Local Similarity
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US-10-286-332A-74
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US-08-207-526-58
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                                                                                                                                  Query Match
                                                        FEATURE:
                                                                                                                                                                    Matches
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APPLICANT: WAIG, Danher TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS FILE REFERENCE: 22488-740
CURRENT APPLICATION NUMBER: PCT/US02/35112
CURRENT FILING DATE: 2002-11-01
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.1
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 119;
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100.0%; Pred. No. 1.1e-17;
ive 0; Mismatches 0;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 90; DB 6;
Pred. No. 8.2e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 100.0%; Score 90; DB il Similarity 100.0%; Pred. No. 8.2 90; Conservative 0; Mismatches
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GENERAL INFORMATION:
                                                                                                                                                                                                               CLAASILICATION: 127
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGIETRATION UNDHER: 35,746
REPERRACIO NUMBER: 19188
TELECOMMUNICATION INFORMATION:
TELEPRAX: (908) 594-3901
TELEPRAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 base pairs
TYPE: mucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 90; Conservative
                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 424
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crccrrgggargrrgargarcrgragrgcr 90

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Sequence 41, Application US/10280915

Sequence 41, Application US/10280915

Sequence 41, Application US/10280915

SEGUENCAL INFORMATION:
TILLE OF INVENTION: MULTIVALENT VACCINATION USING RECOMBINANT ADEMOVIRUS

TILLE OF INVENTION: WUMBER: US/10/280,915

CURRENT APPLICATION NUMBER: US/09/885,599

PRIOR APPLICATION NUMBER: PCT/US01/18238

PRIOR APPLICATION NUMBER: PCT/US01/18238

PRIOR PILING DATE: 2001-06-02

PRIOR APPLICATION NUMBER: PCT/US01/18238

PRIOR PILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-11-01

NUMBER: OF SEQ ID NOS: 75

SOFTWARE: Patentin version 3.1

SEQ ID NO 41

LENGTH: 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arcagagricaaggagaaaatarcagcactrgriggagarggggggggggagarggggggcaccarg 60
Sequence 41. Application US/10003035
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: GENERIC VACCINE AGAINST HUMAN INMUNODEFICIENCY VIRUS
FILE REFERENCE: 22488-712
CURRENT APPLICATION NUMBER: US/10/003,035
CURRENT FILING DATE: 2001-11-01
PRIOR FILING DATE: 2000-66-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 75
SUGTWARE: PATCHELIN VERSION 3.1
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Best Local Similarity 100.0%; Score 90; DB 48; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 90; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 486;
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ORGANISM: Human immunodeficiency virus type 1
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       US-10-003-035-41
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LENGTH: 486
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                                                                                STATEM THEORY WATGY Danher

JAPPILCANT: WATGY DANHER

TITLE OF INVENTION: METHOD OF VACCINATION THROUGH SEROTYPE ROTATION

FILE REPRENCE: 22468-738

CURRENT APPLICATION NUMBER: US/10/266,332A

CURRENT FILING DATE: 2003-03-17

PRIOR APPLICATION NUMBER: US 09/585,599

PRIOR PRILING DATE: 2000-06-04

PRIOR FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-11-01

PRIOR FILING DATE: 2001-11-01

NUMBER OF SEQ ID NOS: 75

SOFFWARE: Patentin version 3.1

SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tabler, Martin
TITLE OF INVENTION: ASYMMETRIC HAMMERHEAD RIBOZOMES AND
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES FOR THEIR CONSTRUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 486;
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,686
FILING DATE: 30-MAY-1996
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PEP94/03391
FILING DATE: 14-OCT-1994
PRIOR APPLICATION NUMBER: EPP3/02853
FILING DATE: 15-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hardaway III, John B.
REGISTRATION NUMBER: 26,554
REGISTRATION NUMBER: 26,554
REGISTRATION NUMBER: 26,554
REGISTRATION NUMBER: 26,554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 90; DB 48;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 90; Conservative 0; Mismatches 0;
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ORGANISM: Human immunodeficiency virus type 1
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hardaway Law Firm
STREET: P.O. Box 10107 Federal Station
CITY: Greenville
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ZIF: 29603-0107
ZIF: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
US-10-286-332A-41; Sequence 41, Application US/10286332A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-628-686-66; Sequence 66, Application US/08628686; GENERAL INFORMATION:
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US-10-286-332A-42
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US-10-280-915-42
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Matches 90
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GENERAL INFORMATION:
APPLICANT: Wang, Danher:
TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
FILE REFERENCE: 22488-712
CURRENT APPLICATION NUMBER: US/10/003,035
CURRENT APPLICATION NUMBER: US/10/003,035
FRIOR APPLICATION NUMBER: 09/585,599
FRIOR APPLICATION NUMBER: PCT/US01/18238
FRIOR APPLICATION NUMBER: PCT/US01/18238
FRIOR APPLICATION NUMBER: PCT/US01/18238
FRIOR APPLICATION NUMBER: PCT/US01/18238
FRIOR PRING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Danher
TITLE OF INVENTION:
GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
TITLE REPREBRENCE: 22488-740
CURRENT APPLICATION NUMBER: PCT/US02/35112
CURRENT APPLICATION NUMBER: US 09/585,599
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR APPLICATION NUMBER: DCT-06-04
PRIOR APPLICATION NUMBER: US 10/003,035
PRIOR APPLICATION NUMBER: US 10/003,035
PRIOR APPLICATION NUMBER: US 10/003,035
NUMBER OF SEQ ID NOS: 75
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100.0%; Pred. No. 1.2e-17;
iive 0; Mismatches 0;
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INFORMATION FOR SEQ 1D NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                      TOPOLOGY: linear // MOLECULE TYPE: CDNA US-08-628-686-66
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Best Local Similarity
Matches 90; Conserval
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Best Local Similarity
Thes 90; Conserve
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PCT-US02-35112-42
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US-10-003-035-42
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Danher
TILE OF INVENTION: MULTIVALENT VACCINATION USING RECOMBINANT ADENOVIRUS
FILE REFERENCE: 22488-741
CURRENT APPLICATION NUMBER: US/10/280,915
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 99/585,599
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 42
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GENERAL INFORMATION:

FILLE OF INVENTION:

FILLE REFERENCE: 22468-738

CURRENT APPLICATION NUMBER: US/10/286,332A

CURRENT FILING DATE: 2003-03-17

FRIOR FILING DATE: 2003-03-17

PRIOR APPLICATION NUMBER: US/10/286,332A

FRIOR FILING DATE: 2000-06-02

FRIOR APPLICATION NUMBER: US/10/03/18238

FRIOR PILING DATE: 2001-06-04

FRIOR PILING DATE: 2001-06-04

FRIOR PELING DATE: 2001-10-01

FRIOR SPELICATION NUMBER: US/10/003,035

FRIOR SPELICATION NUMBER: US/10/003,035

FRIOR SECULIARIES FOUL-10-01

NUMBER OF SECULIARIES PATENTION-11-01

NUMBER OF SECULIARIES PATENTION-11-01
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                                                                                                                                                                                    100.0%; Score 90; DB 43;
100.0%; Pred. No. 1.2e-17;
iive 0; Mismatches 0;
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                                                                                                     ORGANISM: Human immunodeficiency virus type US-10-003-035-42
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 615
                                                                                                                                                                                                                                         90; Conservative
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Best Local Similarity
Matches 90; Conserv
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JATURANT: Wang, Danher

TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN INMUNOBERICIENCY VIRUS
FILE REFERENCE: 22484-740
CURRENT APPLICATION NUMBER: PCT/US02/35112
CURRENT FILING DATE: 2002-11-01
FRIOR APPLICATION NUMBER: PCT/US01/18238
FRIOR FILING DATE: 2001-06-02
FRIOR FILING DATE: 2001-06-04
FRIOR PRICATION NUMBER: PCT/US01/18238
FRIOR FILING DATE: 2001-06-04
FRIOR PRICATION NUMBER: US 10/003,035
FRIOR PRILING DATE: 2001-01
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.1
LENGTH: 786
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100.0%; Score 90; DB 1; Length 786;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 90; Conservative 0; Mismatches 0; Indels
SEQ ID NO 42
LENGTH: 615
TYPE: DNA
ORGANISM: Human immunodeficiency virus type 1
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PCT-US02-35112-47
; Sequence 47, Application PC/TUS0235112
; GENERAL INFORMATION:
                                                                                            US-10-286-332A-42
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March 11, 2004, 18:52:43; Search time 562.569 Seconds (without alignments) 6934.037 Million cell updates/sec
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                                                                                                                                            1 atgagagtgaaggagaaata......tgttgatgatctgtagtgct
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                              nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a

PAT 07-0CT-1996

linear

DNA

ALIGNMENTS

120806 105 bp Sequence 14 from patent US 5516657.

GI:1601161

120806 120806.1

DEFINITION ACCESSION

RESULT 1 120806 LOCUS Unclassified.

Unknown

ORGANISM

KEYWORDS SOURCE

JERSION

AUTHORS TITLE JOURNAL

REFERENCE

1 (bases 1 to 105)
Murphy, C.I. and Young, E.
Baculovirus vectors for expression of secretory and membrane-bound

proteins Patent: US 5516657-A 14 14-MAY-1996:

120806 Sequence 14 108400 Sequence 1 AF051948 HIV-1 iso S77533 rev, vpu [h score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description SUMMARIES HIV1U12030 HIV1U12031 AF358143 AF358145 AF051948 S77533 AF358148 AF201085 AF189159 AY426110 AR382020 HIVH3BH8 AY426115 AR035189 BD182664 AR360240 AR360242 AY426114 HIVHXB3 AR094661 6 I20806 E01088 14 14 14 14 DB 3563 3563 3807 6031 8560 8560 8932 8933 8933 2696 Length 3563 691 Query 00000 100.0 0.00 100.0 100.0 Score Result ģ

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Zhang, Y.-J. and Wadell, G.
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HIV-1 isolate BC9101 from China, vpu pseudogene, complete sequence.
AF051948
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Essex,M.E. and Lee,T.-H.
ASSAY FOR DETECTIONG INPECTION BY HUMAN T-CELL LYMPHOTROPHIC VIRUS
Patent: WO 8602930-A 1 22-MAX-1986;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGAGAGTGAAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 60
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Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
1 (bases 1 to 430)
Li,Q.G., Zhang,Y.J., Liang,Y., Feng,C.Q., Li,Y.Z., Sjoberg,R.,
Jiang,Y., wang,N.F. and Wadell,G.
The morphogenesis of a Chinese strain of HIV-1 forming inclusion
bodies in Jurkat-tat III cells
J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 9 (2), 103-113
                                                                                                                                                                             69
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                                                                                        th 100.0%; Score 90; DB 6; Length 10 Similarity 100.0%; Pred. No. 2e-17; 90; Conservative 0; Mismatches 0; Indels
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                                             /mol_type="unassigned DNA"
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/organism="unknown"
      Location/Qualifiers
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2 (bases 1 to 430)
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Matches 90;
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AF051948
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877533 tev, vpu [human immunodeficiency virus type 1 HIV-1, BC9101, Chinese isolate, Genomic RNA Mutant, 430 nt].
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Li, O.G., Zhang, Y.J., Liang, Y., Feng, C.Q., Li, Y.Z., Sjoberg, R., Jiang, Y., Wang, N.F. and Wadell, G.
The morphogenesis of a Chinese strain of HIV-1 forming inclusion bodies in Jurkat-tat III cells
J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 9 (2), 103-113 (1995)
Li,Q.-G., Zhang,Y.-J. and Wadell,G.
Direct Submission
Submitted (02-MAR-1998) Virology, Umea University, Umea S-901 85,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenBank staff at the National Library of Medicine created this entry [NCB1 gibbsq 165679] from the original journal article. This sequence comes from Fig. 9.

Location/Qualifiers
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Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
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Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 90; Conservative 0; Mismatches 0; Indels
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/organism="Human_immunodeficiency virus 1"

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Pred. No. 2e-17;
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                                                                                                                                                                                              /db xref="taxon:11676"
/ceIl line="Jurkat-tat III"
/country="China"
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/codon_start=1
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/gene="rev"
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93. .341
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Matches

g ò 8 DEFINITION

LOCUS

RESULT 5. AF358148

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE

REFERENCE AUTHORS

JOURNAL

JOURNAL

FEATURES

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/ LTAIRSTALL CSATEKLWITYYGUPWRWGPWILLGMLMICSATEKLWVTVYGVPV
WKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLVNVTENFNWKNDMYB
WKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLVNVTENFNWKNDMYB
WHEDDISLWDQSLKPCYKLPPLVSRDATDTATTLFCANFORSERWMERGERIKNCSFN
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FMDNAKTIIVQLNTSVEIGNETRESNATTRRIBLGROFGRAFTWAKKTGOMRRAHOLIS
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GLLLTRDGGKGNNBSSEIFRPGGGDMRDNWRSELYKVKVVKIEPLGYAATKARKRVVQR
                                                                                                                                                                                                                                                  2 (bases 1 to 1537)
Stipp, H.L., Kumar, A. and Narayan, O.
Direct Submission
Submitted (O2-NOV-1999) Microbiology, Molecular Genetics and
Submitted (O2-NOV-1999) Microbiology, Molecular Genetics and
Immunology, University of Kansas Medical Center, 3901 Rainbow Blvd,
Ransas City, KS 66160, USA
Location/Qualifiers
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Simian-Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
1 (bases 1 to 1577)
Stipp, H.L., Kumar, A. and Narayan, O.
Characterization of immune escape viruses from a macaque immunized
                                                                  lentivirus group.

1 (bases 1 to 1537)
Stipp, H.L., Kumar, A. and Narayan, O.
Characterization of immune escape viruses from a macaque immunized with live-virus vaccine and challenged with pathogenic SHIVKU-1 AIDS Res. Hum. Retroviruses 16 (15), 1573-1580 (2000)
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Simian-Human immunodeficiency virus strain KU-1/105w98 envelope
glycoprotein (env) gene, partial cds.
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              Simian-Human immunodeficiency virus
Simian-Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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/protein_id="AAF13718.1"
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1 (bases 1 to 470)

Atman-Onal,Y., Cheynet,V. and Verrier,B.

Mutations and transcriptional alterations associated with the downregulation of HIV-1 envelope glycoprotein expression following acute cytopathic effects
                                                                                                                                                                                                                                                                                                                  HIV-1 isolate C8-470 from France mutant envelope protein, complete sequence; and nef protein (nef) gene, partial cds.
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Unpublished
2 (bases 1 to 470)
Ataman-Onal,Y., Cheynet,V. and Verrier,B.
Ataman-Onal,X., Cheynet,V. and Verrier,B.
Direct Submission
Submitted (09-MAR-2001) UMR 2142 CNRS/BioMerieux, CERVI-IFR74, 21
Avenue Tony Garnier, Lyon, Rhone 69365, France
Location/Qualifiers
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                                                                                     /product="nef protein"
/protein_id="nAR49980.1"
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/translation="WGGKWSKSSVIGGPTVRERMRRAEPAADRVGAASRDLEKHG"
                                             1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 60

    .470
/note="mutated envelope protein due to large deletion"

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Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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AF201085 GI:6470322
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  Mismatches
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/db_xref="taxon:11676"
/ce]1_line="HL60"
/country="France"
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VRL 27-OCT-2000

DEFINITION ACCESSION VERSION

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PAT 17-AUG-2003

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1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCCACCATG
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Paoletti,E., Tartaglia,J., Cox,W.I., Gallo,R. and Franchini,G. Immunodeficiency recombinant poxvirus
Patent: US 6596279-A 141 22-UUL-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                          Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 2028)
1 (bases 1 to ratedla.J., Cox,W.I., Gallo,R. and Franchini,G. Paoletti,E., Tarteglia.J., Cox,W.I., Gallo,R. and Franchini,G. Immunodeficiency recombinant poxvirus
Patent: Uscation/Qualifiers
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Sequence 138 from patent US 6596279.
AR360240.
AR360240.1 GI:33767121
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/mol_type="genomic DNA"
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FMDNAKTIIVQLNTSVEINCTRPDNNTIKRIRIQRGPGRAFVTMGKIGDMRRAHCNIS
RAKMNDTLKOIASKLAEQFGNNKTIIFKQSSGGDPEIVTHSPNCGGEFFYCNSTQLEN
STAFNSTWSTFSNNTEGSGTITLPCRIKQIINWWQKVGKAMYAPPISGQIRCSSNIT
GLLLTRDGGKGNNESEIFRPGEGDMRDNWGSELYKYKVVKIEPLGVAPTKAKRKVVQR
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WKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPORVVLVNVTENFNWWKNDMVE
OWHEDIISLWDQSLKPCVKLTPLCVSLNCTDLKNDTNTNSSSGGMIMEEGEIKNCSFN
ISTSIRGKVQKEYAFFYKLDIVPIDNDTTSYSLTSCNTSVISQACPKVSFEPIPIHYC
                                                                  Stipp, H.L., Kumar, A. and Narayan, O.
Stipp, H.L., Kumar, A. and Narayan, O.
Direct Submission
Submitted (03-NOV-1999) Microbiology, Molecular Genetics and
Immunology, University of Kansas Medical Center, 3901 Rainbow Blvd,
Kansas City, KS 66160, USA
Location/Qualifiers
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Unclassified.
Unclassified.
1 (bases I to 2020)
Paoletti,E., Tartaglia,J., Cox,W.I., Gallo,R. and Franchini,G.
Immunodeficiency recombinant poxvirus
Patent: US 6596279-A 135 22-JUL-2003;
Location/Qualifiers
with live-virus vaccine and challenged with pathogenic SHIVKU-1
AIDS Res. Hum. Retroviruses 16 (15), 1573-1580 (2000)
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protein_id="AAF13720.1"
db_xref="G1:6470327"
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AR360238
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/organiem="Simian-Human in
/mol_type="genomic DNA"
/strain="KU-1/105w98"
/db_xref="taxon:57667"
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/mol_type="genomic DNA"
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gene="env"
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Matches 90; Conserv
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Best Local Similarity
Matches 90; Conserv
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VERSION
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PAT 17-AUG-2003

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organism="Human immunodeficiency virus 1"
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LaBranche, C.C., Hoffman, T.L., Romano, J., Haggarty, B.S.,
Edwards, T.G., Mathwes, T.J., Doms, R.W. and Hoxie, J.A.
Boterminants of CD4 independence for a human immunodeficiency virus
type 1 variant map outside regions required for coreceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J (bases 1 to 2563)
LaBranche,C.C., Hoffman,T.L., Romano,J., Haggarty,B.S.,
Edwards,T.G., Matthews,T.J., Doms,R.W. and Hoxie,J.A.
Bobited Submission
Submitted (23-SEP-1999) Surgery, Duke University, 117 SORF, LaSalle
Street Extension, Durham, NC 27710, USA
Location/Qualifiers
1. .2563
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2563 bp DNA linear VRL 17-JAN-2000 HIV-1 strain IIIBx clone $10 envelope polyprotein variant (env) gene, complete cds.

AF189159.1 GI:6707314
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1 (bases 1 to 2563)

Hoffman, T. L., Labranche, C. C., Zhang, W., Canziani, G., Robinson, J., Chalken, T. L., Hoxie, J.A. and Dome, R. W.
Stable exposure of the coreceptor-binding site in a CD4-independent
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                                                                                     PAT 02-DEC-1994
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Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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Rusche, J., Lynn, D., Carson, H., Putney, S. and Jellis, C.L.
Recombinant HIV envelope proteins produced in insect cells
Patent: BP 0272858-A2 8 29-JUN-1988;
Location Qualifiers
1. 2552
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Proc. Natl. Acad. Sci. U.S.A. 96 (11), 6359-6364 (1999)
                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 90; DB 6; Length 2552; 100.0%; Pred. No. 1.9e-17; ive 0; Mismatches 0; Indels
                                                                                     linear
                                                                                     DNA
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J. virol. 73 (12), 10310-10319 (1999)
   357 CTCCTTGGGATGTTGATGATCTGTAGTGCT 386
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                                                                                                                                                                                                                                                                                                                    /organism="unknown"
/mol_type="unassigned DNA"
                                                                                   105789 2552 bp
Sequence 8 from Patent EP 0272858.
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RDGGNINNIBESEI FRPGGGDNEDIWREBLYKKYVVKI EPLGYAPTKAKRRYVQREKRAV
GIGALFLGFLGAAGSTWGAASMALTVQARQSLSGI VQQQINLLIRAI EAQQHLLQLTVW
GYGYQLQRI ILAVERYLKDQQLLGIWGCSGKLI CTTAYFWASANSINKSLEQINNINMTWM
EWDREINNYTSLIHSLIESONQQEMNEQELLELDKWASLWWFDI SSWLWYIKI FIN
IVGGJNGLRI VFAVEVVNR RQGYSPLSFCTHLPIPKGFDRPKRIINTYLGRSABPV
PLQLPPLERLTLDCNKD"
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HIV-1 isolate BaL from USA envelope glycoprotein (env) gene,
complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mrvkekkyohlmrmgmrmgtmllgmlmicsateklmvtvyygvpv
wkratttlrcasdakayetevhnvmathacvptdpnpopevylvnvtenrnmwkndmve
omhediislmdoslkpcvkltplcvslkctdlkndtntnsssgrmimekgeikncsfn
istskrgkvkkeyaffykldiipidndptsytltscntsvitgacpkvsffpidihyc
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FTDNAKTI IVOLNTSYBINCTKPNNYTRKRIRIQRGPGRAFYTVGKIGNRQAHONIS
RAKMSNTLKQIASKLREQFONKTI IFKQSGGDPEIVTHSFNCGGEFFYCKSTOLFN
STWSTKGSNNTFGSDTITLPCRIKQIINMWQEVEKAMYAPPISGCIRCSSNIGGLIT
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1 (Dases 1 to 2568)

Pastore, C., Ramos, A. and Mosier, D.E.

Coreceptor switching by HIV-1 is impeded by loss of fitness
Unpublished

2 (Dases 1 to 2568)

Pastore, C., Ramos, A. and Mosier, D.E.

Direct Submission

Submitted (02-007-2003) Dept. of Immunology, The Scripps Research
Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                           /note="can use CXCR4 in a CD4-dependent manner by luciferase-based gene reporter fusion assay and virus infection assay"
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Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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    2568
/organism="Human immunodeficiency virus 1"

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                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/produc===nuvelope polyprotein variant"
/protein_id="AAF25628.1"
/db_xref="GI:6707315"
                                                                                                                                 /cell_line="chronically infected SupT1"
1. .2274
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Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 90; Conservative 0; Mismatches 0;
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'proviral
'mol_type="genomic DNA"
'strain="IIIBx"
                                                                                      'db xref="taxon:11676"
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                                                                                                                                                                                                                                            1. .2274
/gene="env"
                                                                                                                       clone="S10
                                                                                                                                                                                                                    'gene="env"
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/ goldon start=1
/product="envelope glycoprotein"
/product="envelope glycoprotein"
/product="envelope glycoprotein"
/product="alan80885.1"
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/db xref="gl:37962868"
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WKRAYTHIRGENOKEYDTENCYPLORVOTEDPWPOGPELENVYTENFNMWANMWE
OMHEDIISLWDQSIKBCVLPLCVTLENCYDLRWYTENGOFELINGSERBEROW
CSFKTTINIRGENOKEYERENGEPCSNVTVPVCTHORTPWYTTORACPKISFEPI
PIHKCAPAGPAILKCHDKKENGKGPCSNVTVPCTTNVGTRPWYTGACPKISFEPI
PIHKCAPAGPAILKCHDKENGFGPOSNKTIVFRASSGGDPEIVTHSFNCGGEFFYCNSTQ
CNLSRAKWNDTLNKTVVIKAEQFGNKTIVFRASSGGDPEIVTHSFNCGGEFFYCNSTQ
LLINTROGPEDNKTVFREVFRAGGONKTIVFRASSGGDPEIVTHSFNCGGEFFYCNSTG
LLINTROGPEDNKTVFREVFRAGGONKDIWRSELLYKVVKIEPLGVAPTKGRRVVQRE
KRAVGIGAVLIGFICAAAGSTWGAASWTLTVQARLLLGSIVQQQNNLLARIEAQQHLLQ
LTVWGIKQLQARVLAVERYLEDQQLIGIWGCSGKLICTTAVPWNASSNRKSINKIWDN
MTWMEWDEINVYTSIIYSIIEBESQNQORKROBELLEDGWASLMNWFEITEMIMYIK
IFMIIGGLIGIRIVFSYLSIMMRKGYSYSLSFQTHLPASSGPDRRGGEERD
RDRSGRLNNGSLALIWDDLARLCLFSYHRLRDLLLIVTRIVEILGRRGWEALKYWWNL
LQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVPUCARGINHIPPRRIEGERILL"
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HIV-1 clone BaL-1A isolate BaL from USA envelope glycoprotein (env)
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(Dases I to 2568)

Pastore, C., Ramos, A. and Mosier, D.E.

Coreceptor switching by HIV-1 is impeded by loss of fitness
Unpublished

(Dases I to 2568)

Pastore, C., Ramos, A. and Mosier, D.E.

Direct Submission

Submitted (02-007-2003) Dept. of Immunology, The Scripps Research
Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA

Location/Qualifiers
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Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0;
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/organism="Human immunodeficiency virus 1"
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/isolate="Bal"
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/gene="env"
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                          /gene="env"
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HIV-1 clone BaL-1p isolate BaL from USA envelope glycoprotein (env)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OWHED I ISLADOSLKPOVKLTPLCVTINCTDLRNATNGNDTNTTSSEREWMGGGEMKN
CSPKLTTNITGKVOKEXPLFPELDLYPDNOSNYRALIGOSCPKISVITOGACEKKISPEP
PSEKLTTNITGKVOKEXPLFPELDLYPDNOSNYRALIGOSTSVITOGACEKKISPEP
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LLITROGGPEDNKTEVPROGGGDMRDNWRSELYKKVVKIEPLIGVAPTKAKRRVVORE
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                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="mrvkekyQhlwrmgwmrwgtmllgmlmicSateklwytvyyGvPv
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Pastore, C., Ramos, A. and Mosier, D.E.
Direct Submission
Submitted (02-007-2003) Dept. of Immunology, The Scripps Research
Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGGCACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /isolation_source="R5X4 mutant of BaL isolated after
multiple passages in CXCR4 expressing cells"
/db_xref="taxon:11676"
/clone="BaL-1p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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1 ( Dases 1 to 2568)

Pastore.C., Randos.A. and Mosier,D.B.

Coreceptor switching by HIV-1 is impeded by lose of fitness
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/mol type="genomic DNA"
/isolate="Bal"
                                 /db_xref="taxon:11676"
/country="USA"
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   isolate="Bal"
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1. .2568
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LQYWSGELKNSAVSLLNATALAVDEGTDRVIEVLIVTRIPELRYMWLL
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Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0

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| ATGAGAGTGAAGAGAAAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGGCACCATG 60

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Search completed: March 11, 2004, 21:24:07 Job time : 565.569 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

using sw model - nucleic search, OM nucleic

March 11, 2004, 18:51:27; Search time 212.202 Seconds (without alignments) 1801.765 Million cell updates/sec Run on:

1 atgagagtgaaggagagaata..........tgttgatgatctgtagtgct 90 US-10-003-035-74 score: Sequence: Perfect Title:

Scoring table:

3373863 segs, 2124099041 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

6747726

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

genesequ2000s:* genesequ2001as:* genesequ2001bs:* N_Geneseq_29Jan04:* 1: geneseqn1980s:* 2: geneseqn1990s:* geneseqn2002s:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES

	ption	01 gp120 sig			•			92 HIV pl7 8	_	'55 Plasmid p	71 HIV-1 p17	193 HIV pl7 m	76 HIV-1 p24	HIV p	HIV	HIV p	HIV-	HIV p1					•	709 COPAK rec
	Description	Adb87801	Add66325	Aat15319	Aat01088	Aan92594	Adb87770	Add66292	Aaq87557	Aaq89755	Adb87771	Add66293	Adb87776	Add66298	Adb87777	Add66299	Adb87764	Add66286	Adb87765	Add66287	Acc70121	Aat04707	Aat 04708	Aat04709
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	Length DB	6 06		105 2	-			486 9	564 2			٠.	786 9	786 9	915 9			1179 9					2028 2	
æ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	06	06	06	06	06	90	90	90	90	90	90	90	90	90	90	90	90	90	90	90	90	90	90
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Aan80949 HIV prote		_	Aav09364 GMCSF/HIV	Aav36264 Human imm	Adb87752 HIV-1 BH1	Add66274 HIV E_mde		Aav09365 HIV-1/CD4			Add66265 HIV clone			Aat04701 pHIV32 fr	Aav58244 Insert re	Aav60252 Insert re		Add66303 Modified	Adb87783 HIV-1 mod	Add66305 Modified	
AAN80949	ADD66283	AAN80948	AAV09364	AAV36264	ADB87752	ADD66274	AAT05127	AAV09365	AAN60128	ADB87743	ADD66265	ADB87750	ADD66272	AAT04701	AAV58244	AAV60252	ADB87781	ADD66303	ADB87783	ADD66305	
2553 1	2562 9	2598 1	2694 2	2730 2	2747 9	2747 9	2945 2	3084 2	3156 1	3157 9	3157 9	3417 9	3417 9	3808 2	3808 2	3808 2	3839 9	3839 9	4040 9	4040 9	
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24	9 17	27	28	53	30	31	32	33	34	35	36	37	38	c 39	c 40	c 41	42	43	44	45	

ALIGNMENTS

BP. ADB87801 standard; DNA; 90 (first entry) 04-DEC-2003 ADB87801; RESULT 1 ADB87801

gp120 signal peptide DNA fragment.

adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial; antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine; pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.

Human immunodeficiency virus 1.

US2002155127-A1.

24-OCT-2002.

01-NOV-2001; 2001US-00003035.

02-JUN-2000; 2000US-00585599. 04-JUN-2001; 2001WO-US018238.

o. (WANG/) WANG

Wang D;

WPI; 2003-182621/18.

New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor antigens.

Claim 21; Page 81; 156pp; English.

This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparastic, protozoacide, cytostatic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against

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infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaxia. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BH10 antigen construct described in the disclosure of the
                                                                                                                                                                                                                          Sequence 90 BP; 22 A; 11 C; 34 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                           invention
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                                                                                 ATGAGAGTGAAGGAGAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 60
                                                         1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGGTGGAGATGGGGCACATG
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  Length 90;
                             Indels
100.0%; Score 90; DB 9; I
100.0%; Pred. No. 7.7e-20;
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                Local Similarity 100.
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  Query Match
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ADD66325 standard; DNA; 90 15-JAN-2004 ADD66325; RESULT 2 ADD6632

BP

virucide, hepatotropic, RNA editing, GP gene, vaccine, immunity enhanced, infidention, infiduenza; Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial virus; herpes simplex virus, human papilloma virus; HIV infection; ds. HIV gp120 signal peptide DNA. (first entry)

immunodeficiency virus. US2003138459-A1. Human

02-JUN-2000; 2000US-00585599. 04-JUN-2001; 2001WO-US018238. 01-NOV-2001; 2001US-00003035. 17-MAR-2003; 2003US-00286332 24-JUL-2003

(WANG/) WANG D.

Wang D;

WPI; 2003-851718/79

Enhancing the immunity of a host to infection of a first and second pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or HIV infections comprises administering to the host a first and a second recombinant ademovirus.

Example; SEQ ID NO 74; 185pp; English.

The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HTV infections. The present sequence is used in the exemplification of the invention.

Sequence 90 BP; 22 A; 11 C; 34 G; 23 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a fragment of a baculovirus vector of the invention. The vectors are for the expression and secretion of foreign optodeins in an insect cell. The vectors comprise a baculovirus promoter operably linked to an insect virus signal peptide coding region from a baculovirus protein. The signal peptide is either the baculovirus protein of signal peptide is either the baculovirus protein of the Autographa californica muclear polyhedrosis virus (AcNNPV) egt gene. The baculovirus vectors can be used to generate recombinant virus for protein expression in Sf9 cells in a back type system. The vectors allow for the production of proteins that are glycosylated and secreted in the late term of infection, when the promoter is most active.
                                                                                                                                                                                                                                                                                                                                                   Baculovirus vector; p67 signal sequence; insect cell; promoter; egt gene; insect virus; Autographa californica nuclear polyhedrosis virus; AcMNPV; Sf9 cell; glycosylated protein production; HIV-1 gpl20; envelope protein;
                                                                  9
                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baculovirus vectors comprising a signal peptide and promoter – for improved expression and secretion of glycosylated proteins, e.g., \rm HIV-1 gpl20, in the late term of Baculovirus infection.
                                                                 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG
                                                                                           1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGGTGGAGATGGGGCACCATG
                                        Gaps
                                        .,
          Length 90;
                                        Indels
                                         0
             Score 90; DB 9;
Pred. No. 7.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "HIV-1 gp120 fragment"
100.0%; Scc...
100.0%; Pred. No. /...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "p67 signal peptide"
100. .105
                                                                                                                         90
                                                                                                                                                     90
                                                                                                                                         61 CICCIIGGGAIGIIGAIGAICIGIAGIGCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Col 21-24; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
10. .105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CAMB-) CAMBRIDGE BIOTECH CORP.
                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92US-00880647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-00029402
                                                                                                                                                                                                                           AAT15319 standard; DNA; 105
                                                                                                                                                                                                                                                                                  (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= b
                                         90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                             pVLBS2p67120 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-251008/25.
P-PSDB; AAR95884.
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-1992;
                                                                                                                                                                                                                                                                                  25-MAR-2003
18-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5516657-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
             Query Match
Best Local S
Matches 90
                                                                                                                                                                                                                                                       AAT15319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young E,
                                                                                                                                                                                                                                        셤
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                                                                                                                9
                                                                                                                                     69
The glycosylated proteins are produced at a much higher level than in previous systems. These vectors can be used to produce HIV-1 gpl20, and other envelope proteins. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                     10 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG
                                                                                                                1 ATCAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                    coordinate expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New poly-cistronic expression construct - for producing antigens immuno-stimulatory gene products useful as vaccines against e.g.
                                                                                                                                                                                                                                                                                                                                   Polynucleotide vaccine; genetic immunisation; coordinate expres
HIV-1; AIDS; human immunodeficiency virus; antigen; immunogen;
vector VlJns; gpl60; promoter; terminator; CMVintA-BGH; ds; ss.
                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 90; DB 2; Length 119; llarity 100.0%; Pred. No. 8.2e-20; Conservative 0; Mismatches 0; Indels
                                                                  100.0%; Score 90; DB 2; Length 105; 100.0%; Pred. No. 8e-20; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 119 BP; 33 A; 16 C; 40 G; 30 T; 0 U; 0 Other;
                                             Sequence 105 BP; 28 A; 14 C; 37 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                              VlJns-gp160IIIB construct junction sequence.
                                                                                                                                                             90
                                                                                                                                                                                 crccrrecearcrrearcarcrerecr 99
                                                                                                                                                              CICCITGGGATGTTGATGATCTGTAGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 23; Page 138; 178pp; English.
                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shiver JW, Perry HC;
                                                                                                                                                                                                                                           AAT01088 standard; cDNA; 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US002633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-00207526
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                           90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-328276/42.
                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hepatitis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                       WO9524485-A2
                                                                                                                                                                                                                                                                                         26-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                               61
                                                                                                                                                                                                                                                                  AAT01088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu MA,
                                                                                           Matches
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Human T-cell lymphotrophic virus type III - useful for detection of human T-cell lymphotrophic virus type III antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= c
/nctag= corresponds to nucleotide sequence 5802 of the
/nuclear genome"
91...210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGCAGGTGGAGATGCGGCACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= a
note= "comprises leader peptide and mature peptide"
                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence for the amino terminal portion of the HTLV-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                  Glycoproteins gp 120 and gp 160; HTLV-III; HTLV-III antibodies;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 210 BP; 59 A; 32 C; 64 G; 55 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 9.5e-20;
Matches 90; Conservative 0; Mismatches 0;
90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CTCCTTGGGATGTTGATGATCTGTAGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lymphotropic virus type III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page ?; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                          envelope region gp 160 and gp 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84US-00670361.
85US-00795974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85CA-00495112
                                                                                                                                                        AAN92594 standard; DNA; 210
                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag=
                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1989-061499/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAN94662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-1985;
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                                                                                                                                                                                                                                                 27-AUG-2003
                                                                                                                                                                                                                                                                                           28-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoassay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-1988
                                                                                                                                                                                                  AAN92594;
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                                                                                                                RESULT 5
                                                                                                                                       AAN92594
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13 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG

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61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90

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This invention describes a novel recombinant adenovirus comprising an HIV the invention describes a novel recombinant adenovirus elicits an immune response directed against the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparastic, protozoacide, cytostatic and immunoamodulatory activity. The recombinant adenoviruses are useful as waccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immuno-eliminators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-Litrian BHIO antigen construct described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGAGAGTGAAGAGAAATATCAGCACTTGTGGAGATGGGGGGTGGAGATGGGGCACCATG 60
                                                                                                                                                                                adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial; antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine; pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 486 BP; 183 A; 79 C; 131 G; 93 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 90; DB 9; I
Pred. No. 1.2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                              41.
                                                                                                                                              HIV-1 p17 secreted form DNA SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 30; Fig 51A; 156pp; English.
                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                           01-NOV-2001; 2001US-00003035
                                                                                                                                                                                                                                                                                                                                                                                                               02-JUN-2000; 2000US-00585599 04-JUN-2001; 2001WO-US018238
                                   ADB87770 standard; DNA; 486
                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-182621/18.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                US2002155127-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (WANG/) WANG
                                                                                                          04-DEC-2003
                                                                                                                                                                                                                                                                                                                                      24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                         ADB87770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang D;
                 ADB8777
RESULT
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Gaps ö

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                                                                                                                           virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced; infection; influenza; Ebola; Marburg; Arbovirus; hepatitis; respiratory syncytial virus; herpes simplex virus; human papilloma virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enhancing the immunity of a host to infection of a first and second pathogenic virus, e.g. influenza, hepathis, respiratory syncytial, or HIV infections comprises administering to the host a first and a second recombinant adenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGAGAGTGAAGAGAAAATATCAGCACTTGTGGAGATGGGGGGTGGAGATGGGGCACCATG
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human T cell lymphotrophic virus type III bases 5819-6382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 486 BP; 183 A; 79 C; 131 G; 93 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 90; DB 9; I
100.0%; Pred. No. 1.2e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCTTGGGATGTTGATGATCTGTAGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; SEQ ID NO 41; 185pp; English.
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ADD66292
ID ADD66292 standard; DNA; 486 BP.
                                                                                                                                                                                                                                                                                                                            02-JUN-2000; 2000US-00585599.
04-JUN-2001; 2001WO-US018238.
01-NOV-2001; 2001US-00003035.
                                                                                                                                                                                                        Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                               17-MAR-2003; 2003US-00286332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ87557 standard; DNA; 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                       (first entry)
                                                                                                     HIV p17 secreted form DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                          infection; da; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                               2003-851718/79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
tes 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ADD66295
                                                                                                                                                                                                                                     US2003138459-A1
                                                                                                                                                                                                                                                                                                                                                                                         (WANG/) WANG D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JAN-1996
                                                                       15-JAN-2004
                                                                                                                                                                                                                                                                   24-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                           ADD66292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     Wang D;
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(HTLVIII) between bases 5819-6382. The region between bases 37-231 of this sequence (bases 585-605 of the HTLVIII sequence) was amplified region between bases 37-231 of this sequence (bases 585-605 of the HTLVIII sequence) was amplified digested with EcoRI and Khol and ligated with the plasmid pBS-UCU (AAQ87563), also digested with EcoRI and Khol, to generate the asymmetric ribozyme construct p(alpha)Y-R2195 (AAQ87565). The plasmid pBS-UCU is generated by modification of the Helix I box site of plasmid pBS-UCU is the oligonucleotide UCU (AAQ87562). This is an example of an asymmetric ribozyme construct generated to recognise and cleave after the Sequence GUC in the target RNA. The construct encodes the asymmetric xibozyme alpha-Y-R2195 (AAQ87567) which cleaves the HTLVIII RNA sequence AAQ87566. The asymmetric ribozyme generated by transcription of the constructs can be used in treatments to suppress endogenous genes of gathogens or pathogens and pathogens generated by transcriptions of the AB HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asymmetric hammerhead ribozyme(s) and constructs - having high catalytic activity and improved specificity, for inactivating target RNA e.g. in
Human immunodeficiency virus; asymmetric; hammerhead; ribozyme; helix I; helix II; loop 2; cleavage site; amplification; PCR; primer; motif; construct; pathogen; retrovirus infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A portion of the human T cell lymphotrophic virus type III sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 564 BP; 198 A; 93 C; 141 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                (FORT-) FORT FOUND RES & TECHNOLOGY HELLAS.
(DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM STIFTUN.
                                                                                                                                                                                                      complement(213..231)
/*tag= b
/note= "binds primer XHOW"
                                                                                                                                                                 /*tag= a
/note= "binds primer_AR6B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity and improved specificity, for iunwanted endogenous genes or pathogens.
                                                                                                                         location/Qualifiere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 7; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                   93WO-EP002853
                                                                                                                                                                                                                                                                                                                                                                                                            93WO-EP002853
                                                                                                                                            37. .53
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sczakiel G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-161795/21
                                                                                                                                                                                                                                                                                      WO9510608-A1
                                                                                                                                                                                                                                                                                                                                                                   15-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1993;
                                                                                                                                          primer bind
                                                                                                                                                                                                   primer_bind
                                                                                                                                                                                                                                                                                                                             20-APR-1995
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                                                                                Synthetic
                                                                                                                         Key
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09
                                                                                                      437 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 496
                                                                      1 ATGAGAGTGAAAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG
                                     Gaps
                                     .
0
100.0%; Score 90; DB 2; Length 564; 100.0%; Pred. No. 1.2e-19; ive 0; Migmatches 0; Indels
                                                                                                                                                                  CTCCTTGGGATGTTGATCTGTAGTGCT 526
                                                                                                                                           CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
                                   90; Conservative
Query Match
Best Local Similarity
                                                                                                                                           61
                                                                                                                                                                             497
                                   Matches
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BP.

AAQ89755 standard; DNA; 564

AA089755

AAQ89755 ID AAQE XX AC AAQE

RESULT

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The partial sequence of the plasmid pAR6 contg. the human T-cell lymphotrophic virus type III (HTLV-III) bases 5819-6382. The sequence was used to generate an asymmetric ribozyme able to cleave the GTC (GUC in RNA) motif at pos. 230-33. The region between bases 37-231 of this sequence was amplified by the primers AAQ89756-8 and replaced the helix I sequence of construct pSE39-stal2 (AAQ89745). The construct generated (planba)Y-R2195; AAQ89761) encodes the ribozyme (alpha)Y-R2195; AAQ89761) encodes the ribozyme at supermetric ribozyme contg. the catalytic site of a hammerhead ribozyme and a shortened helix I sequence. The ribozymes constructed are asymmetric in that they contain serially deleted Helix I sequences (see AAT05772-80 for other examples). By interchanging the helix I and III sequences, the specificity of the ribozymes can be the seed to inactivate or suppress target RNAs in prokaryote or eukaryote cells such as suppressing certain fruit ripening genes or as protective agents against fungal or insect pathogens
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                                                                   Hammerhead ribozyme; catalytic site; helix; asymmetric; specificity; HIV; prokaryote; eukaryote; fruit ripening gene; protective agent; fungus; virus; insect pathogen; transgenic plant; transformed organism; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asymmetric hammer:head ribozymes - and corresp. coding constructs, for inactivation or suppression of target genes, e.g. in pathogens during fruit ripening.
                                                                                                                                                                                                                                                                   /*tag= b
/note= "binds primers XHOW (AAQ89757) and XHOM
(AAQ89758)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 564;
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                                   Plasmid pAR6 partial seq. contg. HTLV-III bases 5819-6382.
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/note= "binds primer ARA6B (AAQ89756)"
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(DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM STIFTUN.
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100.0%; Pred. No. 1.2.
:ive 0; Mismatches
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                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Fig 7A; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               94WO-EP003391.
08-FEB-1996 (first entry)
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nes 90; Conservative
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RESULT 10 ADB87771

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The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes
                                                                                                                                           virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced; infoction; infiluenza; Ebola; Marburg; Arbovirus; hepatitis; respiratory syncytial virus; herpes simplex virus; human papilloma virus; HIV infection; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enhancing the immunity of a host to infection of a first and second pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or HIV infections comprises administering to the host a first and a second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 90; DB 9; Ler
Pred. No. 1.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or human papilloma virus or HIV infectio
in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CICCITGGGATGTTGATGATCTGTAGTGCT 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; SEQ ID NO 42; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 90; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUN-2000; 2000US-00585599.
04-JUN-2001; 2001WO-US018238.
01-NOV-2001; 2001US-00003035.
                                                                                                                                                                                                                                                         Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-2003; 2003US-00286332
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                                                         (first entry)
                                                                                                    HIV p17 membrane form DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinant adenovirus.
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                                                         15-JAN-2004
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                  ADD66293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            simplex is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang D;
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigan, where expression of the HIV antigan by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparasitic, protozoacide, cytostatic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or B or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immunostimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BH10 antigen construct described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGAGAGTGAAGGAGAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 60
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                                                                                                                                                                                                                                    adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial; antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine; pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
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100.0%; Pred. No. 1.3e-19
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                                                                                                                                                                                           HIV-1 p17 membrane form DNA SEQ ID 42.
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                                                           ADB87771 standard; DNA; 615 BP.
                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2001; 2001US-00003035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-2000; 2000US-00585599.
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Matches 90; Conserv
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Length 615;

infections. The present sequence

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adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial; antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;

ADD66293 standard; DNA; 615 BP.

RESULT 11 ADD66293 ID ADD6

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WPI; 2003-851718/79.
P-PSDB; ADD66301.
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                                   24-JUL-2003
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                                                                                                                                                          Wang D;
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                                                                                                                                                                                                                                                                                                              This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparastic, protozoacide, cytostatic and immunoomidatory activity. The recombinant adenoviruses are useful as infection of apathogenic antigen, e.g. HIV, Ebola virus, hepatilis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or useful as genetic vaccines against pathogenic bacteria, parasites or brotozoans, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-istrain BH10 antigen construct described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced; infection; influenza; Ebola; Marburg; Arbovirus; hepatitis; respiratory syncytial virus; herpes simplex virus; human papilloma virus; HIV infection; ds; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
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pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 786 BP; 280 A; 146 C; 198 G; 162 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 90; DB 9; I 100.0%; Pred. No. 1.3e-19;
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                     Human immunodeficiency virus 1.
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                                                                                              01-NOV-2001; 2001US-00003035
                                                                                                                    02-JUN-2000; 2000US-00585599
04-JUN-2001; 2001WO-US018238
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Best Local Similarity
Matches 90; Conserv
                                               US2002155127-A1
                                                                                                                                                         (WANG/) WANG D.
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                                                                       24-OCT-2002
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                                                                                                                                                                                                                                                                     antigens
                                                                                                                                                                                 Wang D;
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The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AFGAGAGTGAAGGAGAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 786 BP; 280 A; 146 C; 198 G; 162 T; 0 U; 0 Other;
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                                                                      02-JUN-2000; 2000US-00585599.
04-JUN-2001; 2001WO-US018238.
01-NOV-2001; 2001US-00003035.
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04-JUN-2001; 2001WO-US018238.
17-MAR-2003; 2003US-00286332.
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This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparasitic, protozoacide, cytostatic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or useful as genetic vaccines against pathogenic bacteria, parasites or protozoansic, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-letrain HHU antigen construct described in the disclosure of the
                                                                                                                                                    New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 915 BP; 314 A; 168 C; 229 G; 204 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                        Claim 30; Page 63; 156pp; English.
                                                                                                  WPI; 2003-182621/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
                                                                                                                                                                                                                                         antigens
                                            Wang D;
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1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCCACATG ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGGCACCATG Gaps **;** Length 915; 0; Indels Score 90; DB 9; L Pred. No. 1.4e-19; 100.0%; Scc. 100.0%; Pred. No. - 0; Mismatches 8 CTCCTTGGGATGTTGATGATCTGTAGTGCT Local Similarity 100. les 90; Conservative 61 Query Match ઠે ద δ

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> ADD66299 standard; DNA; 915 (first entry) 15-JAN-2004 ADD66299

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BP.

virucide, hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced; infection; influenza; Ebola; Marburg; Arbovirus; hepatitis; respiratory syncytial virus; herpes simplex virus; human papilloma virus; HIV p24 membrane form DNA. HIV infection; ds; gene.

Human immunodeficiency virus.

US2003138459-A1

24-JUL-2003

02-JUN-2000; 2000US-00585599. 04-JUN-2001; 2001WO-US018238. 01-NOV-2001; 2001US-00003035. 17-MAR-2003; 2003US-00286332

(WANG/) WANG

WPI; 2003-851718/79. P-PSDB; ADD66302

Wang

Enhancing the immunity of a host to infection of a first and second pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or HIV infections comprises administering to the host a first and a second recombinant adenovirus.

Example; SEQ ID NO 48; 185pp; English.

The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, bebla, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence is used in the exemplification of the invention.

Sequence 915 BP; 314 A; 168 C; 229 G; 204 T; 0 U; 0 Other;

Gaps ; Length 915; Indels 100.0%; Score 90; DB 9; I 100.0%; Pred. No. 1.4e-19; 0; Mismatches Local Similarion hes 90; Conservative Query Match Matches

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Search completed: March 11, 2004, 20:49:40 Job time : 214.202 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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using sw model nucleic search, OM nucleic March 11, 2004, 18:51:27; Search time 254.642 Seconds (without alignments) 1801.765 Million cell updates/sec Run on:

US-10-003-035-25 Title: Perfect score:

108 l tgtacaagacccaacaacaa.....atatgagacaagcacattgt 108 Sequence:

Scoring table:

3373863 segs, 2124099041 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

N_Geneseq_29Jan04:*

1: geneseqn1980s:*

3: geneseqn200s:*

4: geneseqn200s:*

5: geneseqn2001bs:*

6: geneseqn2001bs:* geneseqn2003as:* geneseqn2003bs:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Adb87754 HIV-1 BH1	Add66276 Multi-cla		Aag04273 Sub 1, a	Aan90623 Sequence	Aag04274 Sub 2, a	Aan92108 Synthetic	Aan90626 N-termina	Aan90739 DNA encod	Aan92116 Polynucle	Aan81450 Sequence	Aan92112 Polynucle	Aaq35897 Recombina	Aan92109 Synthetic	Aan90740 DNA encod	Aan92117 Polynucle	Aan90738 DNA encod	Aan92115 Polynucle	Aan92107 Synthetic	Acc70121 Nucleotid	Aan90741 DNA encod	Aan92118 Sequence	Aan92110 Synthetic
DI DI	ADB87754	ADD66276	AAN90622	AAQ04273	AAN90623	AAQ04274	AAN92108	AAN90626	AAN90739	AAN92116	AAN81450	AAN92112	AAQ35897	AAN92109	AAN90740	AAN92117	AAN90738	AAN92115	AAN92107	ACC70121	AAN90741	AAN92118	AAN92110
DB	9	σ	7	(1	Н	N	Н	Н	Н	Н	Н		~	П	-	7	Н	Н	Н	7	Н	Н	н
Length	108	108	288	288	423	423	536	536	537	537	702	702	702	1056	1059	1059	1269	1269	1276	1533	1791	1791	1796
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Aan81452 Sequence	Adb87745 HIV-1 str	Add66267 HIV clone	Aan81451 Sequence	Adb87761 HIV-1 BH1	Add66283 Modified	Adb87753 HIV-1 BH1	Add66275 HIV E m/E	Aan81449 Sequence	Adb87752 HIV-1 BH1	Add66274 HIV E_mde	Aat05127 HIV vīrus		Add66273 HIV E mde	Adb87743 HIV-1 str	Add66265 HIV clone	Adb87750 HIV-1 BH1	Add66272 HIV Env m	Adb87781 HIV-1 mod	~	Adb87783 HIV-1 mod	AAACCOOF MOGIFIED
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AAN81452	ADB87745	ADD66267	AAN81451	ADB87761	ADD66283	ADB87753	ADD66275	AAN81449	ADB87752	ADD66274	AAT05127	ADB87751	ADD66273	ADB87743	ADD66265	ADB87750	ADD66272	ADB87781	ADD66303	ADB87783	1000000
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1920	2280	2280	2457	2562	2562	2583	2583	2673	2747	2747	2945	2950	2950	3157	3157	3417	3417	3839	3839	4040	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	000
108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	0
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	
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ALIGNMENTS

RESULT 1

HIV-1 BH10 V3 loop clade B SEQ ID 25. ADB87754 Btandard; DNA; 108 (first entry) 04-DEC-2003 ADB87754; ADB8775

adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial; antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine; pathogen; Ebola virus; hepatitis virus; tumour antigen; ds. Human immunodeficiency virus 1. US2002155127-A1.

24-0CT-2002.

02-JUN-2000; 2000US-00585599. 01-NOV-2001; 2001US-00003035. (WANG/) WANG D.

Wang D;

WPI; 2003-182621/18.

New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or B, or tumor antigens.

Claim 17; Fig 48; 156pp; English.

This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparastic, protozoacide, ortostatic and immunomodulatory activity. The recombinant demoviruses are useful as vaccines for eliciting immune response or conferring protection against

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Gaps

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Indels

Length 108;

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1 TGTACAAGACCCAACAATACAAGAAAAGTATCCGTATCCAGAGAGGACCAGGGAGA
                                                                                 1 TGTACAAGACCCAACAACAATACAAGAAAAAGTATCCGTATCCAGAGAGGACCAGGGAGA
                                                                                                                                  61 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
                                                                                                                 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT
                                                                                                                                                                                                                                                                                                                                                                    HIV; AIDS; Sub 1 fusion protein; HIV vaccine; ds.
100.0%; Score 108; DB 9;
100.0%; Pred. No. 7.8e-22;
ive 0; Mismatches 0;
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/label= HIV derived sequence
                                                                                                                                                                                                                                                                                                                                       Sequence encoding Subl HIV fusion protein.
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 Query Match 100.
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Matches 108; Conservative
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Petro J, Okeeffe T;
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Matches 108; Conserv
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infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BHIO antigen construct described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced; infection; influenza; Ebola, Marburg; Arbovirus; hepatitis; respiratory syncytial virus; herpes simplex virus; human papilloma virus;
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                                                                                                                                                                                                                                                                GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
                                                                                                                                                Length 108;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 108 BP; 48 A; 18 C; 23 G; 19 T; 0 U; 0 Other;
                                                                                                                   BP; 48 A; 18 C; 23 G; 19 T; 0 U; 0 Other;
                                                                                                                                              100.0%; Score 108; DB 9; 100.0%; Pred. No. 7.8e-22;
                                                                                                                                                                            o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in the exemplification of the invention.
                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; SEQ ID NO 25; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multi-clade HIV V3 loop clade B.
                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUN-2000; 2000US-00585599.
04-JUN-2001; 2001WO-US018238.
01-NOV-2001; 2001US-00003035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAR-2003; 2003US-00286332
                                                                                                                                                                                                                                                                                                                                                                     ADD66276 standard; DNA; 108
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-851718/79.
                                                                                                                                                            Local Similarity
les 108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003138459-A1
                                                                                                                 Sequence 108
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                                                                                                                                                                                                                                                                                                                                                                                                 ADD66276;
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                                                                                                                                              Query Match
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Grimaila R, Lynn

Jayaherian K, Farley J,

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                                                                                                              Protein derivative stimulates a lymphocyte proliferative response in HIV-
infected humans, providing a means of diagnosis, protection and
therapeutic value. (Updated on 25-MAR-2003 to correct PR field.) (Updated
on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             174
                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTACAAGACCCAACAATACAAGAAAAAGTATCCGTATCCAGAGAGGACCAGGGAGA
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prophylaxis or
HIV infection.
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0
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                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                   Sequence 288 BP; 106 A; 57 C; 67 G; 58 T; 0 U; 0 Other;
New HIV proteins and peptide(s) - used in diagnosis, therapy of AIDS, esp. for prepn. of vaccines against
                                                                                                                                                                                                                                                                                                           100.0%; Score 108; DB 1;
ilarity 100.0%; Pred. No. 9.2e-22;
Conservative 0; Mismatches 0;
                                                                        Claim 1; Table 2; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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Protein derivative stimulates a lymphocyte proliferative response in HIV-fifected humans, providing a means of diagnosis, protection and therapeutic value. (Updated on 25-wAR-2003 to correct PR field.) (Updated on 25-WAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prophylaxis or
HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                  Grimaila R,
  175 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 423 BP; 162 A; 74 C; 89 G; 98 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and peptide(s) - used in diagnosis, esp. for prepn. of vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                  Jayaherian K, Farley J,
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                                                                                                                                                                                 dв.
                                                                                                                                                                                 HIV; AIDS; Sub2 fusion protein; HIV vaccine;
                                                                                                                                                                                                                                                        /*tag= a
/label= HIV derived sequence
                                                                                                                                                          Sequence encoding Sub2 HIV fusion protein.
                                                                                                                                                                                                                              Location/Qualifiers
91. .408
                                                                                                                                                                                                         Simian-Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New HIV proteins and peptide(s) therapy of AIDS, esp. for prepn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Table 3; 29pp; English
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                                                              BP.
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                                                           AAN90623 standard; DNA; 423
                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Rusche JR, Putney SD,
Petro J, Okeeffe T;
                                                                                                           (revised)
                                                                                                                       (revised)
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                                                                                                                                                                                                                                                                                                                                                                                          (REPK ) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1989-070387/10.
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                                                                                                                                                                                                                                             Misc_feature
                                                                                                                                                                                                                                                                                                                                           25-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                   27-AUG-1987;
                                                                                                                      25-MAR-2003
22-JUN-1990
                                                                                                           24-OCT-2003
                                                                                                                                                                                                                                                                                                                   08-MAR-1989
                                                                                                                                                                                                                                                                                           EP306219-A.
                                                                                     AAN90623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                    RESULT 5
AAN90623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 TGTACAAGACCCAACAATACAAGAAAAGTATCCGTATCCAGAGGACCAGGGAGA 174
                                                                                                                                                                   protein; Sub 1; therapy; AIDS; principal neutralising domain; diagnosis; prophylaxis; 8s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The gene can be expressed in simian cells, and synthesis of HIV proteins can be detected immunologically. The recombinant protein product comprises a principal neutralising domain. The neutralising domain is bounded by cysteine residues which occur at positions 296 and 331, the segments between the residues form a loop. See also AAR04427-R04506 and AAQ04273-Q04279. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGTACAAGACCCAACAACAATACAAGAAAAAGTATCCGTATCCAGAGACCAGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Principal neutralising domain of HIV variants - used for producing peptide(s) and antibodies for diagnosis, prophylaxis and/or therapy therapy of HIV infection.
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0
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175 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grimaila R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 288 BP; 106 A; 57 C; 67 G; 58 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                     fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Farley J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 108; DB 2;
100.0%; Pred. No. 9.2e-22;
ive 0; Mismatches 0;
                                                                                                                                            Sub 1, a HIV fusion protein encoding sequence
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/label= HIV portion
                                                                                                                                                                                                                            Location/Qualifiers
1. .288
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                                                                                                                                                                                                                                                                  "HIV
                                                           BP.
                                                                                                                                                                                                                                                                /product= "HIV
/note= "Sub 1"
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89US-00359543.
89US-00407663.
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                                                           288
                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108; Conservative
                                                                                                                                                                                                                                                                                         .253
                                                           AAQ04273 standard; DNA;
                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Putney SD, Petrobre J;
                                                                                                           (revised)
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P-PSDB; AAR04492.
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                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-1988;
01-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                      19-SEP-1989;
                                                                                                         25-MAR-2003
20-SEP-1990
                                                                                                                                                                   HIV; fusion antibodies;
                                                                                                                                                                                                                                                                                                                                        WO9003984-A
                                                                                                                                                                                                                                                                                                                                                                19-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rusche JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PI field.)
                                                                                                                                                                                                       Synthetic.
                                                                                   AAQ04273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lynn DU,
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Matches 10
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Lynn D;

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Region

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It is a synthetic fragment which encodes a portion of HTLV-III gpl20 envelope protein. It has a blunt end on the 5' end and a CTAG overhang on the non-coding strand at the 3' end which will ligate with BamHI. Used in example to construct pPB1 which is used to express the recombinant HTLV-III fusion protein PB1. PB1 is used to stimulate lymphocyte proliferative response in HTLV-III infected humans. It is suggested that PB1 can be used in the diagnosis, prophylaxis or therapy of AIDS. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGTACAAGACCCAACAATACAAGAAAAAGTATCCGTATCCAGAGAGGACCAGGGAGA
                                                      Synthetic polynucleotide encoding HTLV-III gp120 envelope protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant human T-cell leukaemia virus 3 proteins - used for stimulating lymphocyte proliferative response and in diagnosis prophylaxis or therapy of AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GCATTIGITACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 108; DB 1; Length 536; larity 100.0%; Pred. No. 1e-21; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 536 BP; 218 A; 86 C; 106 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                   Mueller WT,
                                                                                        HTLV-III envelope protein gp120; pPB1; PB1; lymphocyte proliferative response; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV; AIDS; env gene; HIV vaccine; ds.
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(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                              (REPK ) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                     Lynn D,
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1989-157957/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-OCT-2003
25-MAR-2003
22-JUN-1990
                                                                                                                                                                                                                                                       18-AUG-1988;
                                                                                                                                                                                                                                                                                              09-0CT-1987;
 10-MAR-2003
02-MAR-1990
                                                                                                                                                                               AU8821172-A
                                                                                                                                                                                                                      13-APR-1989
                                                                                                                                                                                                                                                                                                                                                                   SD,
                                                                                                                                               Synthetic.
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                                                                     HIV; fusion protein; Sub 2; therapy; AIDS; principal neutralising domain; antibodies; diagnosis; prophylaxis; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The gene can be expressed in simian cells, and synthesis of HIV proteins can be detected immunologically. The recombinant protein product comprises a principal neutralising domain. The neutralising domain is bounded by cysteine residues which occur at positions 296 and 331, the segments between the residues form a loop. See also AAR0427-R04506 and AAQ04273-Q04279. (Updated on 25-WAR-2003 to correct PR field.) (Updated on 25-WAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTACAAGACCCAACAACAATACAAGAAAAAGTATCCGTATCCAGAGAGGACCAGGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Principal neutralising domain of HIV variants - used for producing peptide(s) and antibodies for diagnosis, prophylaxis and/or therapy therapy of HIV infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 GCATTTGTTACAATAGGAAATAGGAAATATGAGACAAGCACATTGT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grimaila R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 108; DB 2; Length 423; Best Local Similarity 100.0%; Pred. No. 9.7e-22; Matches 108; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 423 BP; 162 A; 74 C; 89 G; 98 T; 0 U; 0 Other;
                                                                                                                                                                                                                  "HIV 18 kD fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Farley J,
                                  fusion protein encoding sequence
                                                                                                                                                                                                                                  /note= "Sub 2"
91. .407
/*tag= b
/label= HIV portion of Sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Javaherian K,
                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page ?; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         88US-00252949.
89US-00359543.
89US-00407663.
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                                                                                                                                                                                                 /*tag= a
/product= '
(first entry)
                                                                                                                                                                                   . 423
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Lynn DU, Petrobre J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPK ) REPLIGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1990-147824/19.
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01-JUN-1989;
19-SEP-1989;
                                  Sub 2, a HIV
                                                                                                                                                                                                                                                                                                                                                                                                      03-OCT-1988;
20-SEP-1990
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EP306219-A

25-MAR-2003

AAN92108;

AAN92108
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61

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Gaps

9 87

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It is an example of a nucleotide sequence coding for a novel protein which is composed of the HIV portion of fusion protein PBI, with or without the N-terminal Met. The novel protein is claimed and so are transfer vectors comprising AAN90740, eg plasmids pdeltaPBI and pd2PBI. BBI is disclosed in EPA 0255190. The novel protein can be used in assays for detecting or quantifying anti-HIV antibody and may be incorporated into vaccine compositions. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       It encodes the HIV portion of HTLV-III fusion protein PB1. PB1 is produced from plasmid pPB1 which contains the HTLV-III env gene from Pvu II - Bg1 II. The protein encoded by this polymucleotide is used to stimulate lymphocyte proliferative response in HTLV-III infected humans.
                            Recombinant HIV proteins - used in assays for detecting and quantifying antibody against HIV and for incorporation into vaccine compsns.
                                                                                                                                                                                                                                                                                                                               1 TGTACAAGACCCAACAACAATACAAGAAAAAGTATCCGTATCCAGAGAGGACCAGGGAGA
                                                                                                                                                                                                                                                                                                                                                               28 IGTACAAGACCCAACAACAATACAAGAAAAGTATCCGTATCCAGGAGGACCAGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide encoding HIV portion of HTLV-III fusion protein PB1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stimulating lymphocyte proliferative response and in diagnosis prophylaxis or therapy of AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                135
                                                                                                                                                                                                                                                                                                                                                                                                61 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
                                                                                                                                                                                                                                                                     DB 1; Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Farley J;
                                                                                                                                                                                                                                                                                                                                                                                                               GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT
                                                                                                                                                                                                                                     Sequence 537 BP; 218 A; 86 C; 106 G; 127 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                     100.0%; Score 108; DB 1; 100.0%; Pred. No. 1e-21;
                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTLV-III envelope gene; HIV; pPB1; lymphocyte proliferative response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Table 13A; Page ?; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lymphotrophic virus typ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87US-00107231.
                                                                         Fig 2; Page ?; 17pp; English
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                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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P-PSDB; AAP93537
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10-MAR-2003
02-MAR-1990
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                                                                                                                                                                                                                                                                                                 108;
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Matches
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                                                                                                                                                                                                                                                                                 Protein derivative stimulates a lymphocyte proliferative response in HIV-
infected humans, providing a means of diagnosis, protection and
therapeutic value. Synthetic proteins AAP90278-83 are derived from this
sequence. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
MAR-2003 to correct PA field.) (Updated on 24-0CT-2003 to standardise OS
field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                            Lynn
                                                                                                                                                                                                      New HIV proteins and peptide(s) - used in diagnosis, prophylaxis or therapy of AIDS, esp. for prepn. of vaccines against HIV infection.
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                                                                                                                           Grimaila R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 536;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV; pdeltaPB1; pd2PB1; transfer vector; immunoadsorbent; vaccine. env gene; HTLV-III; fusion protein PB1.
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 536 BP; 218 A; 86 C; 106 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 108; DB 1; Length 5:
100.0%; Pred. No. 1e-21;
ive 0; Mismatches 0; Indels
                                                                                                                           Farley J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding HIV portion of fusion protein PB1
                                                                                                                           Jayaherian K,
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                                                                                                                                                                                                                                                    Disclosure; Page ?; 29pp; English.
                             88EP-00307889
                                                           87US-00090080
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Best Local Similarity 100.0
Matches 108, Conservative
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                                                                                                                         , Putney SD, Okeeffe T;
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                                                                                         (REPK ) REPLIGEN CORP
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08-JUN-1990
08-MAR-1989
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                                                                                                                                          Petro J,
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It is suggested that this protein can be used in the diagnosis, prophylaxis or therapy of AIDS and for the preparation of vaccines against HTLV-III. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                               Immunoassay; AIDS vaccine; antigen; immunogen; diaqnostic; HIV; LAV; ds.
                                                                                                                                      TGTACAAGACCCAACAACAATACAAGAAAAAGTATCCGTATCCAGAGAGGACCAGGGAGA
                                                                                                      Gaps
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                                                                                                                                                                  GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
                                                                                  Length 537;
                                                                                                                                                                               GCATTTGTTACATAGGAAAATAGGAAATATGAGACAAGCACATGT
                                                                                                                                                                                                                                                                                                                         Sequence encoding fusion protein PB1 of HTLV-III envelope
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                                                             Sequence 537 BP; 218 A; 86 C; 106 G; 127 T; 0 U; 0 Other;
                                                                                                     0; Indels
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                                                                                 100.0%; Score 108; DB 1; 100.0%; Pred. No. 1e-21;
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                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Human T-cell Lymphotropic virus type
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1. .702
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(revised)
(first entry)
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P-PSDB; AAP81143.
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                                                                                            Similarity
                                         correct PA field.)
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06-DEC-1990
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                                                                                 Query Match
                                                                                            Local
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Recombinant DNA transfer vectors which comprise all or part of the uncleotide sequence or equiv. contg. bases whose translated region codes for the R10, PB1, 590 or KH1 fragments of HTLV-II envelope protein. Host cells transformed with these vectors and HTLV-III envelope protein fragments R10, PB1, 590 and KH1 are claimed. These protein fragments are useful in immunoassays for detection of HTLV-III antibodies; as antignic components of A1DS vaccines; also to stimulate lymphocyte proliferative response in infected individuals. (Updated on 25-MAR-2003 to correct PA 2003 to corre

Sequence 702 BP; 260 A; 129 C; 148 G; 165 T; 0 U; 0 Other;

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                                                                          115 TGTACAAGACCCAACAACAACAATACAAGAAAAGTATCCGTATCCAGAGAGACCAGGGAGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              It encodes a protein called PBI (26kD) which is an HTLV fusion protein produced from pPBI. pPBI contains the HTLV-III env gene from Pvu II - Bgl II. The HIV portion of PBI is used to stimulate lymphocyte proliferative response in HTLV-III infected humans. It is suggested that the HIV portion can be used in the diagnosis, prophylaxis or therapy of AIDS and for the preparation of vaccines against HTLV-III. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PP field.)
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                                Gapa
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                                                                                                              61 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
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1larity 100.0%; Pred. No. 1.1e-21;
Conservative 0; Mismatches 0;
    Score 108; DB 1;
Pred. No. 1.1e-21;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Table 9A; Page ?; 85pp; English.
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    100.0%;
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Unidentified.
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Query Match
Best Local Similarity 100.
Matches 108; Conservative
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Best Local S:
Matches 108,
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02-MAR-1990 (first entry)
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Best Local Similarity 100.(
Matches 108; Conservative
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                                                                                                                                                                                       Lynn D,
                                                                                                                                                                                                          WPI; 1989-157957/22.
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                                                                     Synthetic.
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                                        HTLV-III
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                                                                                                                                                                                                                                                                                                                                             New recombinant HIV envelope protein PB1 - for treatment, prevention and diagnosis of HIV and AIDS.
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                                                                                                                                                      Human immunodeficiency virus; HIV; envelope protein; AIDS; ds.
 108
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                175 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT
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                                                                                                                                                                                                                                                                                                Farley
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100.0%; Pred. No. 1.1e-21;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                               Mueller WT,
                                                                                                                                   Recombinant PBI fusion protein gene.
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                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 12; 18pp; English.
                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAN92109 standard; DNA; 1056
                                                                                                                                                                                                                                    92EP-00116879
                                                                                                                                                                                                                                                       86US-00892680
                                                                 AAQ35897 standard; DNA; 702
                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
Les 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                          (REPK ) REPLIGEN CORP
                                                                                                                                                                                                                                                                                               Lynn D,
                                                                                                                                                                                                                                                                                                                WPI; 1993-038178/05
                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR31943
                                                                                                                                                                                                                                    19-JAN-1987;
                                                                                                                                                                                                                                                       01-AUG-1986;
                                                                                                       25-MAR-2003
02-JUN-1993
                                                                                                                                                                                              EP525828-A2
                                                                                                                                                                                                                03-FEB-1993
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10-MAR-2003
                                                                                                                                                                                                                                                                                              Putney SD,
                                                                                                                                                                           Synthetic
                                                                                    AAQ35897;
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ID AAN9
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AC AAN9
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DT 25-M
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It is a synthetic fragment which encodes a portion of HTLV-III gpl60 envelope protein. It has a blunt end on the 5' end and a TCGA overhang on the mon-coding strand at the 3' end which will ligate with HindlII. Used in example to construct p590 which is used to express recombinant HTLV-III fusion protein 590. 590 is used to stimulate lymphocyte proliferative response in HTLV-III infected humans. It is suggested that 590 can be used in the diagnosis, prophylaxis or therapy of AIDS. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PP field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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Synthetic polynucleotide encoding HTLV-III gp160 envelope protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stimulating lymphocyte proliferative response and in diagnosis prophylaxis or therapy of AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV; p590; pdeltaPBl; pd2PBl; transfer vector; immunoadsorbent; vaccine. env gene; HTLV-III; fusion protein 590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 108; DB 1; Length 1056; 100.0%; Pred. No. 1.1e-21; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GCATTIGITACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1056 BP; 384 A; 177 C; 255 G; 240 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding HIV portion of fusion protein 590
                                                                HTLV-III envelope protein gp160; p590; 590; lymphocyte proliferative response; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .1059
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Table 6; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                           88AU-00021172.
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It is an example of a nucleotide sequence coding for a novel protein which is composed of the HIV portion of fusion protein 590, with or without the N-terminal Met. The novel protein is claimed and so are transfer vectors comprising AAN9740, eg plasmids pdeltarB1 and pd22P1. 590 is disclosed in EPA 0255190. The novel protein can be used in assays for detecting or quantifying anti-HIV antibody and may be incorporated into vaccine compositions. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                     Recombinant HIV proteins - used in assays for detecting and quantifying antibody against HIV and for incorporation into vaccine compsns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1059 BP; 384 A; 180 C; 255 G; 240 T; 0 U; 0 Other;
                                                                                                                                                                                     Farley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 108; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 108; Conservative 0; Mismatches 0;
                                                                                                                                                                                   Mueller WT,
                                                                                                                                                                                   Javaherian K,
                                                                                                                                                                                                                                                                                                                       Fig 3; Page ?; 17pp; English.
                                                                                   88EP-00302695
                                                                                                                   87US-00107703
                                                                                                                                                  (REPK ) REPLIGEN CORP
                                                                                                                                                                                                                   WPI; 1989-108200/15.
P-PSDB; AAP93538.
                                                                                                                                                                                     Lynn D,
                                                                                 25-MAR-1988;
                                                                                                                   09-OCT-1987;
                                                 12-APR-1989
                EP311228-A.
                                                                                                                                                                                     Putney SD,
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Search completed: March 11, 2004, 20:49:38 Job time : 259.642 secs

GCATTIGITACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 135

61 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108

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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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March 11, 2004, 20:30:23 ; Search time 54.4954 Seconds (without alignments) 1099.812 Million cell updates/sec Run on:

US-10-003-035-25 108 Title: Perfect score:

1 tgtacaagacccaacaacaa...........atatgagacaagcacattgt 108 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

682709 Begs, 277475446 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

/cgn2_6/ptodata/2/ina/5A_COMB.seq:*/cgn2_6/ptodata/2/ina/5B_COMB.seq:*/cgn2_6/ptodata/2/ina/6A_COMB.seq:*/cgn2_6/ptodata/2/ina/ed=COMB.seq:*/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*/cgn2_6/ptodata/2/ina/bcackfiles1.seq:*/ Issued Patents NA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Patent No. 5462872	ce 1.	4	m	Sequence 4, Appli	ď	4,	18	Sequence 18, Appl	18,	18	18	Sequence 3, Appli	7	7	,	7	22	25,	18,	Sequence 1, Appli	9	Sequence 1, Appli	7	13	Н	'n,
SOFTWARTES	5462872-1	US-09-124-900-1	-210-	9	-09-620-9	-95	US-08-463-028-4	US-08-459-818-18	-889	US-08-465-078-18	US-08-725-776-18	US-08-488-062-18	US-07-916-098A-3	08-589-	US-08-444-882-7	US-08-389-459A-7	US-08-987-867A-7	98-	US-08-530-146-25	-07-956-4	US-07-916-098A-1	US-08-472-240A-9	US-08-147-890-1	US-08-147-890-2	08-037-8	08-530-146-	US-08-188-583-5
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* Query Match	100.0	100.0	100.0	100.0			100.0	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5	98.5
Score	108	108	108	108	108	108	108	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4	106.4
Result No.		7	٣	4	ß	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

	Sequence 800, App Sequence 800, App Sequence 43, Appl
US-08-388-353-1 US-08-488-551B-1 US-09-718-096-15 US-09-718-096-15 US-09-700-304-1 US-08-318-138-13 US-08-646-538-35 US-09-503-222-35 US-09-503-222-35 US-08-78-122-1 US-08-78-122-1 US-08-78-122-1 US-08-78-122-1 US-08-463-028-6 US-08-337-387-4	US-08-388-353-800 US-08-488-551B-800 US-09-646-028-43
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2 4 4 4 4 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9	4 4 4 4 5

ALIGNMENTS

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1153 TGTACAAGACCCAACAACAATACAAGAAAAGTATCCGTATCCGGAGAGACCAGGGGGA 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
                 ; APPLICANT: Jonak, Zdenka L.; Debouck, Christine; Clark, Robert; Trulli, Stephen
                                                             Trulli, Stephen

TITLE OF INVENTION: HUMAN LYMPHOID CELLS EXPRESSING HUMAN
IMMUNODEFICIENCY VIRUS ENVELOPE PROTEIN GP160
NUMBER OF SEQUENCES: 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/08/134,128
FILING DATE: 08-0CT-1993
PRIOR APPLICATION NUMBER: 906,613
FILING DATE: 30-10N-1992
APPLICATION NUMBER: 587,011
FILING DATE: 24-SEP-1990
                                                                                                                                                                                                                                                                                                                                                             ; SEQ ID NO:1:
; LENGTH: 2945
5462872-1
;Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                             5462872-1
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1213 GCATTIGITACAATAGGAAAATAGGAAATATGAGACAAGCACATIGT 1260 Sequence 1, Application US/09124900 Patent No. 6268484 GENERAL INFORMATION: APPLICANT: SCHMATZ, Christine APPLICANT: KLIMA, Annelies APPLICANT: STEINDL, Franz APPLICANT: MUSTER, Thomas TITLE OF INVENTION: HIV-Vacci BALLAUN, Claudia PURTSCHER, Martin TRKOLA, Alexandra PREDL, Renate KATINGER, Hermann BUCHACHER, Andre ERNST, Wolfgang US-09-124-900-1 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: 셤

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NAME/KEY: mat_peptide
LOCATION: 4367..4975
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LOCATION: 5560..8148
                                            ORGANISM: HTLV-III
                  ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-620-958A-3
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US-08-463-210-4
; Sequence 4, Application US/08463210
; Patent No. 6001977.
; Patent No. 6001977.
; APPLICANT: CHANG, Nancy T.
; APPLICANT: CHANG, Robert C.
; APPLICANT: GALLO, Robert C.
; TITE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
; TORRESPONDENCES 11
; CORRESPEE Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 8932;
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CUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,210
FILING DATE: 05-UN-1995
CLASSIFICATION: 436
PRIOR APPLICATION NUMBER: US/06/693,866
FILING DATE: 23-UAN-1995
FILING DATE: 23-UAN-1995
FILING DATE: 10-OCT-1984
ATFORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-OCT-1984
ATFORMEY/AGENT INFORMATION:
TELEPRANTON NUMBER: 35,353
REGISTRATION NUMBER: 35,353
REGISTRATION NUMBER: 35,353
FERRENCE/DOCKET NUMBER: 2026-4193US2
TELEPRANTON NUMBER: 35,353
REGISTRATION NUMBER: 35,353
REGISTRATION NUMBER: 35,353
REGISTRATION NUMBER: 35,353
REFERENCE/OPCKET NUMBER: 35,353
REGISTRATION NUMBER: 35,353
RESPRENCE/DOCKET NUMBER: 35,353
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 30,353
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 30,353
REGISTRATION NUMBER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 108; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 108; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Human imunodeficiency virus type 1
US-09-124-900-1
                                                                                                           PCT/EP95/01481
FILE REFERENCE: 1939-112P
CURRENT APPLICATION NUMBER: US/09/124,900
CURRENT FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: PCT/EP95/01481
PRIOR FILING DATE: 1995-04-19
                                                                                                                                                                          NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 8932
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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6466 TGTACAAGACCCAACAATACAAGAAAAGTATCCGTATCCAGAGAGACCAGGGAA 6525
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NAME/KEY: misc_feature
LOCATION: 1..8933
OTHER INFORMATION: / Standard_name= "Clone BH10"
OTHER INFORMATION: / note= "Corresponds to nucleotide positions 222 to OTHER INFORMATION: 9154 in figure 3 of EP 85307260"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGTACAAGACCCAACAACAATACAAGAAAAAGTATCCGTATCCAGAGAGACCAGGGAGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)...(8933)
CTHER INFORMATION: Sequence of transcripts produced from the BH10
PARTENT NO. 6294338
CTHER INFORMATION: plasmid.
US-09-620-9588-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 108; DB 3; Length 8933; Best Local Similarity 100.0%; Pred. No. 2.5e-24; Matches 108; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GCATTIGITACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09620958A

Patent No. 629438

GENERAL INFORMATION:
APPLICANT: Nunomura, Kiyotada
TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
FILE REPRENCE: GP104-02.UT
CURRENT APPLICATION WOMBER: US/09/620,958A

NUNBER OF SEQ ID NOS: 9
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 3
IENGTH: 8933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Human Immunodeficiency Virus
FRATURE:
NAME/KEE: 6017C6
                                                                                                                                                                                                                                                                                NAME/KEY: mat peptide
LOCATION: 1408..4452
OTHER INFORMATION: /product= "pol"
                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 4367.4975
OTHER INFORMATION: /product= "sor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 5560. 8148
; OTHER INFORMATION: /product= "env"
US-08-463-210-4
                                                                                                                                           FEATURE:
NAME/KEX: mat peptide
LOCATION: 113..1648
OTHER INFORMATION: /product= "gag"
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g

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NAME/KEY: mat_peptide
LOCATION: 4367..4975
OTHER INFORMATION: /product= "sor"
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OTHER INFORMATION: /product= "pol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: mat_peptide
LOCATION: 113.1648
OTHER INFORMATION: /product= "gag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: mat peptide LOCATION: 1408..4452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: HTLV-III FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE
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6526 GCAUUUGUUACAAUAGGAAAAUAGGAAAUAUGAGACAAGCACAUUGU 6573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 108; DB 3; Length 8933; Best Local Similarity 82.4%; Pred. No. 2.5e-24; Matches 89; Conservative 19; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 108; DB 3; Length 8933; Best Local Similarity 82.4%; Pred. No. 2.5e-24; Matches 89; Conservative 19; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Sequence of the IAC-Bscr pseudo target; patent No. 6294338
; NAME/KEY: mutation; 10CATION: (4140)...(4159)
; OTHER INFORMATION: Mutated positions: 4140-42, 4145-47, 4152, 07HER INFORMATION: 4156-57, 4159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence 9, Application US/09620958A
| Patent No. 6294336
| GENERAL INFORMATION:
| APPLICANT: Nunomura, Kiyotada
| TILE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
| FILE REFRENCE: GP104-02.UT
| CURRENT APPLICATION NUMBER: US/09/620,958A
| CURRENT FILING DATE: 2000-07-21
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 9
| LEMGTH: 8933
                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Sequence of the IAC-Asrc pseudo target
                                                                                                                                                                 APPLICANT: NUMBER: X KIYOtada
TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
FILE REFERENCE: GP104-02. UT
CURRENT APPLICATION NUMBER: US/09/620,958A
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 8933
                                                                                    US-09-620-958A-4
Sequence 4, Application US/09620958A
Patent No. 6294338
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-09-620-958A-9
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NAME/KEY: misc_feature
LOCATION: 1..8933
COTHER INFORMATION: / Standard_name= "Clone BH10"
OTHER INFORMATION: /note= "Corresponds to nucleotide positions 222 to
OTHER INFORMATION: 9154 in figure 3 of EP 85307260"
                                                                                                                                                    RESULT 7
US-08-463-028-4
; Sequence 4, Application US/08463028
; Patent No. 610476
; GENERAL INFORMATION:
; APPLICANT: CHANG, Nancy T.
; APPLICANT: GALLO, Robert C.
; APPLICANT: MONG-STREES II
; CORRESPONDENCES: II
; CORRESPONDENCES: MOTGAN & Finnegan, L.L.P.
; STREET: 345 Park Avenue
COURRESPONDENCE ADDRESS:
SUDRESSEE: Morgan & Finnegan, L.L.P.
STREE: 345 Park Avenue
CITY: New York
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: LIBM PC COMPATIBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: DAY FORM: DC-DOS/MS-DOS
SOFTWARE: IBM PC COMPATA:
MEDIUM TYPE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 05-UN-1995
CLASSIFICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-CCT-1984
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 35,353
REFERENCE/CATION NUMBER: 35,35
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Sequence 18, Application US/08465078;
Patent No. 5885796;
GENERAL INFORMATION:
APPLICANT: Linaley, Peter S.
APPLICANT: Danle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Brady, William
APPLICANT: Riener, Peter A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                             Sequence 18, Application US/08899666 Patent No. 5885579 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: DNA (genomic) US-08-889-666-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 781 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                    61 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
                                                                                                                                         Query Match
100.0%; Score 108; DB 4; Length 8933;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 108; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/08459818
Patent No. 5851795
GENERAL INFORMATION:
APPLICANT: Linaley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Longer Nitin K.
APPLICANT: Longer Nitin K.
APPLICANT: Longer Nitin K.
APPLICANT: Longer Nitin K.
APPLICANT: CTLA4 Receptor and Uses Thereof NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30436,35US02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSeq 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,818
FILING DATE: 02-UN-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 34,470
TELECHONE: 310-445-1140
TELECHORE: 310-445-1140
; FEATURE:
NAME/KEX: mat_peptide
LOCATION: 5560..8148

OTHER INFORMATION: /product= "env"
US-08-463-028-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.1<sup>1</sup>
Matches 107, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 781 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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US-08-459-818-18
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US-08-459-818-18
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1 TGTACAAGACCCAACAACAATACAAGAAAAGTATCCGTATCCAGAGAGGACCAGGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Riener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof NUMBER OF SEQUENCES: 26
CORRESPONDERS: ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 08-JUL-1997

CLASSIFICATION 1435

PRIOR APPLICATION 1435

PRIOR APPLICATION 1985

CLASSIFICATION 1985

PILING DATE: 18-JAN-1995

CLASSIFICATION: 435

PILING DATE: 18-JAN-1995

CLASSIFICATION: 435

APPLICATION NUMBER: US 08/375390

FILING DATE: 18-JAN-1995

CLASSIFICATION: 435

APPLICASIFICATION: 435

TELESSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 30436-35US01

TELEPHONE: 310-445-1140

TELEPHONE: 310-445-1140

TELEPACC CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 98.5%; Score 106.4; DB 2; Best Local Similarity 99.1%; Pred. No. 4.2e-24; Matches 107; Conservative 0; Mismatches 1;
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563 TGTACAAGACCCAACAACAATACAAGAAAAGTATCCGTATCCAGAGGGGACCAGGGAGA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 781;
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Sequence 18, Application US/08488062
Sequence 18, Application US/08488062
Fatent No. 5977318
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nithin K.
APPLICANT: Riener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,062
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATIORNEY, AGENT INFORMATION:
          Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 98.5%; Score 106.4; DB 2; Best Local Similarity 99.1%; Pred. No. 4.2e-24; Matches 107; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30436-35US01
                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                          NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 781 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Riopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
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REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-725-776-18
                                                                                                               FILING DATE
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98.5%; Score 106.4; DB 2; Length
Best Local Similarity 99.1%; Pred. No. 4.2e-24;
Matches 107; Conservative 0; Mismatches 1; Indels
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Patent No. 5968510

GENERAL INFORMATION:

APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Brady, William K.
APPLICANT: Riener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COMPURSY: USA
ZIP: 9025
COMPURSY: USA
ZIP: 9025
                                                                                                                                                                                                     STATE: Caliborna

COUNTRY: USA

ZIP: 90025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,078

FILING DATE: 18-JAN-1995

PRIOR APPLICATION 435

PRIOR APPLICATION OF SATA B:

APPLICATION NUMBER: 34,70

REFERENCE/DOCKET NUMBER: 30436-35US01

TELECOMMUNICATION NUMBER: 30436-35US01

TELECOMMUTCATION NUMBER: 
CTLA4 Receptor and Uses Thereof
                 NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                 CITY: Los Angeles
STATE: California
FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-08-725-776-18
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874 TGTACAAGACCCAACAACAATACAAGAAAAAGAATCCGTATCCAGAGAGGACCAGGGAGA 933
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                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                               Length 1497;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      934 GCATTIGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT 981
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Sequence 7, Application US/08589446

Patent No. 5614410.

GENERAL INFORMATION:

APPLICANT: MOTIOW, CASEY D.

TITLE OF INVENTION: ENCAPSIDATED POLIOVIRUS NUCLEIC

TITLE OF INVENTION: USING SAME

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                         Query Match

98.5%; Score 106.4; DB 2;
Best Local Similarity 99.1%; Pred. No. 5e-24;
Matches 107; Conservative 0; Mismatches 1;
                                                             ANTICATION CONTROL OF THE PRATURE:

NAME/KEY: CDS

LOCATION: 1.1494

PEATURE:

NAME/KEY: misc_feature

LOCATION: 1

COCATION: 1

OTHER INFORMATION: /note= "soluble HIV gp120"
US-07-916-098A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,446
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESGEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/087,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Geary III, William C.
REGISTRATION NUMBER: 31,359
REFERENCE/DOCKET NUMBER: UAG-C
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 base pairs
TYPE: NUMBER: SIGIE
STRANDENNESS: SIGIE
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                      MOLECULE TYPE:
HYPOTHETICAL: 1
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, LOCATION:
US-08-589-446-7
  TOPOLOGY:
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Patent No. 5871732
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: HOWAS, DAVID W.
APPLICANT: ROSA, WARGARET D.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, USSEPH J.
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USFFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INPECTION
                                                                                                                                                                                                                                                                                                                                                                                                             563 TGTACAAGACCCAACAATACAAGAAAAAGTATCCGTATCCAGAGGGGGCCCAGGGAGA 622
                                                                                                                                                                                                                                                                                                                                                            1 TGTACAAGACCCAACAACAATACAAGAAAAAGTATCCGTATCCAGAGAGGACCAGGGAGA 60
                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                 DB 2; Length 781;
                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                              98.5%; Score 106.4; DB 2; 99.1%; Pred. No. 4.2e-24; tive 0; Mismatches 1,
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ZIP: 66066
COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION ATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION NUMBER: 92,499
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION NUMBER: 92,310-G
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION NUMBER: 92,949
REFERENCE/DOCKET NUMBER: 92,949
REFERENCE/DOCKET NUMBER: 92,910-G
TELEPAN: (312) 715-1200
TELEFAN: (312) 715-1200
TELEFAN: (312) 715-1200
TELEFAN: 1010 D NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1497 base pairs
TYPE: NUMBER: Airs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
            INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 781 bases pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-488-062-18
310-445-1140
                                                                                                                                                                                                                                                              Query Match 98.5;
Best Local Similarity 99.1;
Matches 107; Conservative
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  TELEPHONE:
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US-07-916-098A-3
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                                                                                                                                                            1 TGTACAAGACCCAACAACAATACAAGAAAAGTATCCGTATCCAGAGAGGACCAGGGAGA 60
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Best Local Similarity 99.1%; Pred. No. 5.1e-24;
Matches 107; Conservative 0; Mismatches 1; Indels 0;
Query Match

98.5%; Score 106.4; DB 1; Length 1568;
Best Local Similarity 99.1%; Pred. No. 5.1e-24;
Matches 107; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                             61 GCATTIGITACAATAGGAAAATAGGAAATATGAGACAAGCACATIGT 108
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Sequence No. 562705

GENERAL INFORMATION:
FREED OF INVENTION:
TITLE OF INVENTION:
TOTAL:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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; LOCATION:
US-08-444-882-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-444-882-7
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Search completed: March 11, 2004, 23:12:13 Job time : 59.4954 secs Н

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Sequence 1, Application US/09124900
Patent No. 6268484
GENERAL INFORMATION:
APPLICANT: KATINGER, Hermann
APPLICANT: BUCHACHER, Andrea
APPLICANT: BRIST, Wollgang
APPLICANT: BALLAUN, Claudia
APPLICANT: FTKOLA, Alexandra
APPLICANT: FTKOLA, Alexandra
APPLICANT: RTKOLA, Alexandra
APPLICANT: RTKOLA, Alexandra
APPLICANT: SCHMATZ, Christine
115581
12581
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LENGIH: 2945
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Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 1, Appli
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                                                                March 11, 2004, 20:30:23 ; Search time 65.0917 Seconds (without alignments) 1099.812 Million cell updates/sec
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                                                                                                                           1 ttattcataatgatagtagg.....acctcccaatcccgagggga 129
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Sequence 9,
Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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/cgn2 6/ptodata/2/ina/6A_COMB.seq:*
/cgn2 6/ptodata/2/ina/6B_COMB.seq:*
/cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-620-58A-3
US-09-620-58A-3
US-08-463-028A-9
US-08-38B-353-651
US-08-38B-353-651
US-09-325-131B-1
US-09-325-131B-1
US-08-418-848A-3
US-08-418-848A-4
US-08-418-848A-5
US-08-418-848A-6
US-08-418-848A-6
US-08-418-848A-7
US-08-38B-551B-1
US-09-309-571B-1
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US-08-935-312-13
US-08-848-760B-33
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                             682709 segs, 277475446 residues
                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             nucleic search, using sw model
                                                                                                                                              IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                      Issued Patents NA:*
                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                       US-10-003-035-75
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Query
Match 1
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                                                                                                                                                Scoring table:
                                              nucleic
                                                                                                                            Sequence:
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2376
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Sequence 615,
Sequence 615,
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Sequence 800,
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Sequence 7,
Sequence 7,
Sequence 7,
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Sequence 3
Sequence 5
Sequence 5
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TILE OF INVENTION: HUMAN LYMPHOID CELLS EXPRESSING HUMAN
TILE OF INVENTION: HUMAN LYMPHOID CELLS
IMMUNOBERICIENCY VIRUS ENVELOPE PROTEIN GP160
NUMBER OF SEQUENCES: 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 18/08/134,128
FILING DATE: 08-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 596,613
FILING DATE: 34-NN-1992
APPLICATION NUMBER: 587,011
FILING DATE: 24-SEP-1990
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US-07-916-098A-1
US-08-147-890-1
US-08-147-890-1
US-08-463-210-6
US-08-463-028-6
US-08-499-446-7
US-08-444-882-7
US-08-989-459A-7
US-08-989-459A-7
US-08-989-882-7
US-08-989-882-7
US-08-988-833-615
US-08-988-333-615
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Best Local Similarity 100.
Matches 129; Conservative
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LENGTH: 8933
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Patent No. 6001977

GENERAL INFORMATION:
APPLICANT: GALLO, Robert C.
APPLICANT: MONG-STAAL, Flossie
TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8932;
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COUNTRY: USA
ZIE: 10154-0053
COMPUTER READBLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
HING DATE: 05-UNN-1995
FILING DATE: 05-UNN-1995
FILING DATE: 05-UNN-1995
FILING DATE: 05-UNN-1995
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 129; DB 3;
Best Local Similarity 100.0%; Pred. No. 5.7e-33;
Matches 129; Conservative 0; Mismatches 0;
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CLASSIFICATION: 436
PION APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-UAN-1985
PRICH APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-OCT-1984
APPLICATION NUMBER: Lealie A.
RESISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 35,353
TEMPERENCE/DOCKET NUMBER: 35,353
TEMPERENCE/DOCKET NUMBER: 2026-4193US2
TEMPERENCE/DOCKET NUMBER: 2026-4193US2
                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA; ORGANISM: Human imunodeficiency virus type 1 US-09-124-900-1
APPLICANT: KLIMA, Annelies
APPLICANT: STEINDL, Franz
APPLICANT: STEINDL, Franz
TITLE OF INVENTION: HIV-Vaccines
FILE REFERENCE: 1939-1129
CURRENT PEDILICATION NUMBER: US/09/124,900
CURRENT FILING DATE: 1998-07-30
PRIOR PILING DATE: 1998-07-30
PRIOR PILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
IENGTH: 8932
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US-08-463-210-4
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7630 ITATICATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCT 7689
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NAME/KAY:

NAME/KAY:

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NOTHER INFORMATION:

OTHER INFORMATION:

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LOCATION: (1)...(8933)
COTHER INFORMATION: Sequence of transcripts produced from the BH10
Patent No. 6294338
OTHER INFORMATION: plasmid.
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TITLE OF INVENTUON: POLYNUCLEOTIDE AMPLIFICATION METHOD
FILE REFERENCE: GP104-02.U US/09/620,958A
CURRENT APPLICATION NUMBER: 2000-07-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FABELSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1408..4452
OTHER INFORMATION: /product= "pol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ); NAME/KEY: mat_peptide
; LOCATION: 5560.8148
; OTHER INFORMATION: /product= "env"
US-08-463-210-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 4367.4975
OTHER INFORMATION: /product= "sor"
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                                                                                 LENGTH: 8933 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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121 CCGAGGGGA 129
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TYPE: nucleic acid
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US-08-463-028-4
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OTHER INFORMATION: Mutated positions: 4135, 4140-1, 4145, 4150,
OTHER INFORMATION: 4152-3, 4155
                                    Query Match 100.0%; Score 129; DB 3; Length 8933; Best Local Similarity 67.4%; Pred. No. 5.7e-33; Matches 87; Conservative 42; Mismatches 0; Indels 0
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OTHER INFORMATION: Sequence of the IAC-Asrc pseudo target
Patent No. 6294338
NAME/KEY: "....." (1725)
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Patent No. 6294338
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
FILE REFERENCE: GF104-02.UT
CURRENT APPLICATION NUMBER: US/09/620,958A
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NUNCHURA, KIYOCAGA
APPLICANT: NUNCHURA, KIYOCAGA
TITLE OF INVENTION: POLIVUCLEOTIDE AMPLIFICATION METHOD
FILE REFERENCE: GP104-02.UT
CURRENT APPLICATION NUMBER: US/09/620,958A
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/09620958A; Patent No. 6294338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 67.49
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                               7750 CCGAGGGGA 7758
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US-09-620-958A-9
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LENGTH: 8933
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US-09-620-958A-4
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JS-09-620-958A-3
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253 ATAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 312
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98.8%; Score 127.4; DB 3; Length 1596;
Best Local Similarity 99.2%; Pred. No. 1.1e-32;
Matches 128; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
COUNTY: ADDRESSER: SCULIY, SCULY, GARREN CITY CARREN CITY COUNTRY: U.S.A.
ZITE: 11530-0299
COMPUTER NEADABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION COMPATION COMPATION COMPATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-REB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: NO0284 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 110-MAPPLE PM41-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 110-MAPPLE PM41-1995
APPLICATION NUMBER: PM3021/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 651, Application US/08488551B
Patent No. 6015661
GENERAL INPORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Diciglio, Frank 2
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-436
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 651:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) US-08-388-353-651
     14-FEB-1995
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                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1.8933
COCHER INFORMATION: /standard name= "Clone BH10"
OTHER INFORMATION: /note= "Corresponds to nucleotide positions 222 to OTHER INFORMATION: 9154 in figure 3 of EP 85307260"
NAME/KEY: mat_peptide
LOCATION: 113.1648
OTHER INFORMATION: /product= "gag"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTTAAGAATAGTTTTTGCTGTACTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Cooper, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City Plaza
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ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide
LOCATION: 1408..4452
OTHER INFORMATION: /product= "pol"
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!CCATION: 5560..8148
. GTHER PRORMATION: /product= "env"
US-08-463-028-4
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OTHER INFORMATION: /product= "sor"
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STRANDEDNESS: single
TOPGLIGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 100.
Matches 129; Conservative
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                                                                                                                                       ORGANISM: HTLV-III
                                                                                                             ORIGINAL SOURCE:
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NAME/KEY:
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APPLICANT: CLOYD, MILES W.
APPLICANT: RAMESY, KEITH
TITLE OF INVENTION: BIA TEST USING NONDENATURED HIV ANTIGEN FOR EARLY
TITLE OF INVENTION: DETECTION OF HIV INFECTION
FILE REFREENCE: UTSG:234
CURRENT APPLICATION NUMBER: US/09/325,1318
CURRENT APPLICATION NUMBER: 08/728,122
PRIOR FILING DATE: 1999-06-08
PRIOR FILING DATE: 1999-10-09
PRIOR FILING DATE: 1993-10-26
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PALENTIN VOY: 2.1
SEQ ID NO 1
LEMBERT OF SEQ ID VOY: 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                            1 TIATICATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCT
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                                                                                                                                                                                                                                                                                                                        DB 3; Length 1596;
                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                      98.8%; Score 127.4; DB 3 99.2%; Pred. No. 1.1e-32;
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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NAME: FRANK S. DIGIGLIO
REFERENCE/POCKET NUMBER: 9606.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
INFORMATION FOR SEQ ID NO: 651: SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-488-551B-651
                                                                                                                                                                                                                                                                                                                                           Similarity
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Best Local
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2579 GIAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTGAGACCCACCTCCCAACC 2638
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                                                                             GENERAL INFORMATION:
APPLICANT: Cloyd, Miles W.
APPLICANT: Rangey, Keith M.
APPLICANT: RANGEY, Keith M.
TITLE OF INVENTION: HIV Antigen for Early Detection of
TITLE OF INVENTION: HIV Antigen for Early Detection of
TITLE OF INVENTION: HIV Infection
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.
STREET: 816 Congress Avenue, Suite 1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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| Patent No. 5847096 | GENERAL INFORMATION:
| APPLICANT: SCHUBERT, MANFRED, HARMISON II,
| APPLICANT: GEORGE G., CHANG-UIE, CHEN, BANJERJEA, AKHIL:
| TITLE OF INVENTION: DEFECTIVE, INTERFERING
| TITLE OF INVENTION: HIV PARTICLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,122
FILING DATE: 09-CCT-1996
CLASSIFICATION: 536
ATTONEY AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: 43424.0003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
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Pred. No. 1.3e-32;
0; Mismatches 1;
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CORRESPONDENCE ADDRESS:
ADDRESSES: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
Sequence 1, Application US/08728122; Patent No. 6074646
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 99.24
Matches 128; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2639 CCGAGGGGA 2647
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US-08-728-122-1
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US-08-418-848A-3
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1981 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCT 2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2041 ATAGTGAATAGGGTAGGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 2100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

98.8%; Score 127.4; DB 2; Length 3426;
Best Local Similarity 99.2%; Pred. No. 1.4e-32;
Matches 128; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08418848A

Patent No. 5847096

GENERAL INFORMATION:
APPLICANT: SCHUBERT, MANFRED, HARMISON II,
APPLICANT: SCHUBERT, MANFRED, HARMISON II,
TITLE OF INVENTION: DEFECTIVE, INTERFERING
TITLE OF INVENTION: HIV PARTICLES
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 345 PARK AVENUE
COUNTRY: U.S.A.
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM DESCRIPTION OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WOND PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,848A FILING DATE: 07-APR-1995
CLASSIFICATION 526
FRIOR APPLICATION DATA:
APPLICATION STATE
FRIOR APPLICATION 526
FRIOR APPLICATION 526
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936,849
FILING DATE: 28-AUG-1992
CLASSIFICATION: 526
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
07/936,849
              FILING DATE: 28-40G-1992
CLASSIFICATION: 526
ATTORNEY TRRORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPHONE: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 202
RELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                       TELEX: 421792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3426 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2101 CCGAGGGGA 2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CCGAGGGA 129
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TELEX: 421792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SCHUBERT, MANFRED, HARMISON II,
APPLICANT: GEORGE G., CHANG-UIE, CHEN, BANJERJEA, AKHIL
TITLE OF INVENTION: DEFECTIVE, INTERFERING
TITLE OF INVENTION: HIV PARTICLES
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: U.S.A.
                   COMPOUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,849A
FILING DATE: 07-APR-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/936,849
FILING DATE: 07-APR-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/936,849
FILING DATE: 28-AUG-1992
CLASSIFICATION SEG
ATTOREY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE: 212-758-4800
TELEFRANCE: 212-758-4800
TELEFRANCE: 212-758-6849
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ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,848A
FILING DATE: 07-APR-1995
CLASSIFRICATION: 5.26
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-418-848A-2; Sequence 2, Application US/08418848A; Patent No. 5847096
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TELEX: 421792
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2940 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid_
STRANDEDNESS: single
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1981 ITATICATAATGATAGTAGGAGCTIGGTAGGTITAAGAATAGTITITGCTGTACTITCT 2040
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98.8%; Score 127.4; DB 2; Length 3480;
Best Local Similarity 99.2%; Pred. No. 1.4e-32;
Matches 128; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08418848A

Patent No. 5847096

GENERAL INFORMATION:
APPLICANT: SCHUBERT, MANFRED, HARMISON II,
APPLICANT: GEORGE G, CHANG-JIE, CHEN, BANJERJEA, AKHIL
TITLE OF INVENTION: HIV PARTICLES
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                  1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTT
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SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,848A
FILING DATE: 07-APR-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/936,849
FILING DATE: 28-AUG-1992
CLASSIFICATION 526
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,459
REFRENCE/DOCKET VUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS.
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3480 base pairs
; TYPE: nucleic acid
; STRANDEDINESS: single
; TOPOLOGY: linear
US-08-418-848A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3721 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: sing
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US-08-418-848A-5
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Gaps

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Query Match

98.8%; Score 127.4; DB 2; Length 3721;
Best Local Similarity 99.2%; Pred. No. 1.5e-32;
Matches 128; Conservative 0; Mismatches 1; Indels 0;

1981 TTATTCATAATCATAGTAGTAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCT 2040 120 9 1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTT Search completed: March 11, 2004, 23:12:15 Job time: 65.0917 secs 2101 CCGAGGGGA 2109 121 CCGAGGGGA 129 g a ò $\overset{\circ}{\sigma}$

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nuc	nucleic search, using sw model
Run on:	March 11, 2004, 18:52:43 ; Search time 806.349 Seconds (without alignments) 6934.037 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-003-035-75 129 1 ttattcataatgatagtaggacctcccaatcccgagggga 129
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272 seqs, 21671516995 residues
Total number of	hits satisfying chosen parameters: 6940544
Minimum DB seq 1 Maximum DB seq 1	length: 0 length: 2000000000
Post-processing:	<pre>: Minimum Match 0% Maximum Match 100% Listing first 45 summaries</pre>
	3: 9b_in:* 4: 9b_om:* 5: 9b_om:* 6: 9b_pat:* 7: 9b_ph:* 9: 9b_pr:* 10: 9b_ro:* 11: 9b_ro:* 11: 9b_sts:* 12: 9b_om:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scription	1	162 8	128 DNA seque	I05789 Sequence 8	55081 Seque	2	Human		_		_	AX078308 Sequence	AX078313 Sequence	E01099 DNA sequenc	X01762 Human T-cel	I07983 Sequence 1	AEA20244 Cimthoria	Artonat ayment	BD238379 Virus vac	AX032757 Sequence	106771 Sequence 8		AY426103 HIV-1 clo	HIV-1	HIV-1	HIV-1	AY4261U/ HIV-1 CLO	1-711	Seguenc	BD000747 Recomembi	AR264703 Sequence	AR097865 Sequence	AR064430 Sequence	AROBA423 Sequence	AROSA431 SEQUENCE	1 10	4	435 Sequenc	380	2758	64436	H		
SUMMARIES	ID	I02160	102162	E02028	105789	AR365081	M			AR09465	AR38201	AX07830	AX078308	AX07831	Щ			HIVEIZCG		α	AX032757	106771								AX166280	BD000747	AR264703	AR097865	AR064430	AK064429	AK064431	AR064432	AR064434	AR064435	BD238380	AX032758	AR064436	HIV1U26942	ALIGNMENTS	
	° Query Match Length DB	861 6		. ~	۵.	2945 6		"	8932 14	_	_	_	8933 6	_	_	_	Δ.		27 27 20 10	^ ~	. ~	2264 6	•	_	2559 14		_	2559 14		2562 6			2730 6	- ·		3480 6		4059 6	~	229	6229 6	399	•		
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PAT 21-MAY-1993

linear

102160 861 bp ss-DNA Sequence 1 from Patent US 4861707. 102160 IO2160.1 GI:270316

RESULT 1 102160 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

inknown.
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 861)
Ivanoff,L.A. and Petteway,S.R.
Human immunodeficiency virus antigen
Patent: US 4861707-A 1 29-AUG-1989;
E. I. Du Pont de Nemours and Company; Wilmington, DE

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PAT 02-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIAGIGAAIAGAGITAGGCAGGGATATICACCATTATCGITICAGACCCACCTCCCAATC 120
                                                                                                                                             C12N7/04, C07K13/00, C12P21/02//A61K39/21, C12N15/00, (C12P21/02,
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                                    Pacent: JP 1999179687-A 1 17-JUL-1989;
CHEMO SERO THERAPEUT RES INST
N JP 198919687-A/1
PD 17-JUL-1989
PF 30-DEC-1987 JP 1987336292
PF 30-DEC-1987 JP 19873418592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 2552)
Rusche, J., Lymn, D., Carson, H., Putney, S. and Jellis, C.L.
Recombinant HIV envelope proteins produced in insect cells
Patent: EP 0272858-A2 8 29-JUN-1988;

    .2130
/product='gag-env hybrid protein' FT

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Nozaki,C., Matsushita,S., Hattori,T. and Takatsuki,K.
HIV FUSED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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100.0%; Pred. No. 4e-28;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                       *source: clone=Plasmid lambdaBH10;
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 129; DB 6;
; Pred. No. 4e-28;
0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
/wol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2552 bp
Sequence 8 from Patent EP 0272858.
105789
                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DN/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                               strandedness: Double;
                                                                                                                                                                                (C12N15/00, C12R1:91)
                                                                                                                                                                                                               topology: Linear;
hypothetical: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                             anti-sense: No;
                                                                                                                                                                                                                                                                                                                                      2131. .2237
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Best Local Similarity 100.
Matches 129; Conservative
                                                                                     PD 17-JUL-1989
PF 30-DEC-1987 JF
PI NOZAKI CHIKAH
TAKATSUKI KIYOSHI
                                                                                                                                                                                                                                                                                                                                                                 1. .2237
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Best Local Similarity
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ACCESSION
VERSION
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AUTHORS
TITLE
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                         TITLE
           AUTHORS
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I05789
                                                                        COMMENT
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DI 198177967-A/1.
Homo sapiens (human)
Homo sapiens
Eukaryotes, Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2237)
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Ivanoff, L.A. and Petteway, S.R.
Human immunodeficiency virus antigen
Patent: US 4861707-A 3 29-AUG-1989;
E. I. Du Pont de Nemours and Company; Wilmington, DE
Location/Qualifiers
                                                                                                        Length 861;
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DNA sequence coding for gag-env hybrid protein.
E02028
                                                                                                                                                                   TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGT
                                                                                                      100.0%; Score 129; DB 6;
100.0%; Pred. No. 4.2e-28;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 102162 10216 bp ss-DNA Sequence 3 from Patent US 4861707.
                                            /organism="unknown"
/wol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="unknown"
           Location/Qualifiers
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Best Local Similarity 100.
Matches 129; Conservative
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Unclassified.
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129; Conserv
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ндунXB3 3156 bp ss-RNA linear VRL 02-AUG-1993
Human immunodeficiency virus type 1, isolate HXB3, env region.
M14100
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Crowl,R., Gardon,M., Conroy,R., Schaber,M., Kramer,R., Shaw,G., Wong-Staal,F. and Reddy,B.P.
HTLV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients
[621 41 (3), 979-986 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC
G01N33/569,G01N33/577, (C12N1/20,C12R1:125), (C12N1/20,C12R1:19), PC
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Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
                                                                                                                                                                                                              /product='HTLV-III envelop protein'
Location/Qualifiers
1. .3156
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/mol_type="genomic RNA"
/db_xref="taxon:11676"
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/note="genomic mRNA"
/1 .3156
/note="tat, rev, nef subgenomic mRNA"</pre>
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100.0%; Pred. No. 3.9e-28;
iive 0; Mismatches 0;
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                                                                   C12R1:125), (C12P21/02,C12R1:19);
strandedness: Double;
tcpology: Linear;
hypothetical: No;
anti-sense: No;
*Source: library=genome library;
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/codon_start=1
/proteIn_id="AAA44675.1"
/db_xref="GI:327752"
                                                                                                                                                                                                                                                                                                   /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Location/Qualifiers
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Best Local Similarity 100.0
Matches 129; Conservative
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                                                         C12P21/02,
C12P21/02,
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Robadro, M.K., Robadto, C.G., Eragamu, P.R., Jiyooji, M.S. and Furct Bunkl. I.U.

ENVELOPE PROTEIN OF VIRUS OF ACCUIRED IMMUNODEFICIENCY SYNDROME
ENVELOPE PROTEIN OF VIRUS OF ACCUIRED IMMUNODEFICIENCY SYNDROME
PROTEIN LA ROCHE & CO AG, USA GOVERNMENT
OS Human (Homo capiens)
PN JP 1987012799-A/1
PD 21-3M1-1987
PF 18-APR-1986 JP 1986089830
PR 19-APR-1986 US 85 725021
PR 19-APR-1985 US 85 725021
PI ROBANTO MITSUCHIERU KUROURU, ROBANTO CHIYAARUZU GARO, PI
ERAGAMU PUNEMURUMAA REDEI, JIYOOJI METSUDO SHIYOU, PI FUROTSUSHII
IICHINGU UONGUUSUTAARU
PC C07K13/00, A61K39/21, C07H21/04, C12N1/20, C12N15/00, C12P21/00, PC
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                                         2095 GTAGTGAATAGAGTTAGGCGAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 2154
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                   GTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 120
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                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 2945)
Jonak, Z.L., Debouck, C., Clark, R. and Trulli, S.
Human lymphoid cells expressing human immunodeficiency virus
envelope protein GP160
Patent: US 5462872-A 1 31-OCT-1995;
Location/Qualifiers
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                                                                                                                                                                                                                             DNA
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Sequence 1 from patent US 5462872.
AR365081
AR365081.1 GI:34428384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
/wol_type="genomic DNA"
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JP 1987012799-A/1.
unidentified
unidentified
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Best Local Similarity 100.
Matches 129; Conservative
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                                                                                             CCGAGGGGA 129
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Unclassified.
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AR365081
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E01088
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Gaps

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Original source text: Human immunodeficiency virus type 1 (HIV-1) proviral DNA clone BH10.

[(in) Weiss_R.Y. Teich, N., Varmus, H. and Coffin, J. (Eds.); RNA Tumor Viruses, Molecul review; bases 1 to 8932.

The BH10 sequence differs from BH8 and BH5 by 0.9% in the coding regions and 1.8% in the noncoding regions, and the authors of [1] believe that these are stable variants.

The HTLV-III genome encodes at least seven proteins: gag, pol, env, tat, trs, 27% antigen and the sor 23% product. The 3' ORF (positions 8153-873) is truncated in BH10 (stop codon at positions 8522-8524), but reads through in BH8 and other sequences to yield what is now called the 27% antigen.

The mechanism for pol gene translation has not been elucidated: a gag-pol fusion protein is possible, splicing or frameshift have not been ruled out. The viral protease would be determined by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region in question.

The Tat protein (trans-activator protein, approximately 14 kb) is an effector of an autostimulatory pathway through interaction with a positive control element, the trans-activating responsive sequence. TAR. Tat seems to be a transcriptional control molecule in HTLV-I, but is both that and a post-transcriptional regulatory molecule in HTLV-III. Deletion mutants in the tat gene are incapable of prolific replication and exhibit no cytopathic effects in T4+ cell lines.

In addition to the addition to th
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Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1148-1152 (1991)
                                                                                                                                                                                                                                                                                                                                                                           HIVBH102 8932 bp ss-RNA linear VRL 02-AUG-1993 Human immunodeficiency virus type 1, isolate BH10, genome. M15654 K02008 K02009 K02010 M15654 I GI:326383
2587 GTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 2646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAR region; acquired immune deficiency syndrome; env protein; gag protein; long terminal repeat (LTR); pol protein; polyprotein; porviral gene; reverse transcriptase; transactivator.

2 of 2
Human immunodeficiency virus 1 (HIV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lentivirus group.
1 (bases 1 to 8932)
Wong-Staal,F., Gallo,R.C., Chang,N.T., Ghrayeb,J., Papas,T.S.,
Wong-staal,F., Paerson,M.L., Petteway,S.R.Jr., Ivanoff,L.,
Lautenberger,J.A., Pearson,M.L., Refalski,J.A., Doran,E.R.,
Baumeister,K., Whitehorn,E.A., Rafalski,J.A., Doran,E.R.,
Josephs,S.J., Starcich,B., Livak,K.J., Patarca,R., Haseltine,W.A.
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van Beveren,C.P., Coffin,J. and Hughes,S.
Appendix B: HTLV-3 genome
Appendix B: HTLV-3 genome
(in) Weiss,R.L., Teach,N., Varmus,H. and Coffin,J. (Eds.);
RNA TUMOR VIRUSES, MOLECULAR BIOLOGY OF TUMOR VIRUSES, SECOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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Cold Spring Harbor Laboratory, CSH, NY (1985)
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                                                                                                                          121 CCGAGGGA 129
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/db_xref="GI:327753"
/db_xref="GI:327753"
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ISYGRKKRRQFRRPPGGSQTHQV5LSKQPTSQSRGDPTGPKE"
join(226. .301,2532. .2906)
/note="rev protein"
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ISTSIRGKVQKEXAFFYKLD I I PI DNDTTSYTLTSCNTSVI TQACPKVSFEPI PI HYC
STSIRGKVQKEXAFFYKLD I I PI DNDTTSYTLTSCNTSVI TQACPKVSFEPI PI HYC
FTDNAKTI I LYCNNKTFNGTGPCTNVSTYQCTHGI RRYVSTQLLLMGSLABEBEV I RSVN
FTDNAKTI I LYCNNKTFNGTGPCRAFYTI KKKI I QKFGRAFYTI GKI GNMRQAHCNI S
RAKNNATLKQI ASKLREQFGNNKTI I FKQSSGGDPEI VTHSPNCGGEFFYCNSTQLFN
STWFNSTWSTEGSNNTEGSDTITLPCRI KQFINMQEVGKAMYAPPI SGQI RCSSNIT
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QUTWWGIKQLQARILAVERYLKDQQILGIWGCSGKLLCTTAVPWNAGASUKSILSQIWN
QUTWWGINDREINNYTSLIHESLIESQNQQEKNEQELLEIDKWASLWWFNITWWLWYI
KLFIMIVGGILGILYYPAVLSVVNRYRQSYSFLSFQTHIPIPERGPEREGGER
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WRERQRQIHSISERILSTYLGRSAEPVPLQLPPLERLTLDCNEDCGTSGTQGVGSPQI
LVESPTILESGAKE"
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LIERAEDSGNESEGEISALVEMGVEMGHAPWDVDDL"
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/note="nef protein, partial"
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/translation="MGGKWSKSSVVGWPAVRERMRAEPAADGVGAASR"
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100.0%; Pred. No. 3.9e-28;
ive 0; Mismatches 0;
                       translation="ILQQLLFIHFQNWVST"
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(db_xref="G1:327755"
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'db_xref="GI:327756"
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/note="tat protein"
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/note="tat protein"
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2586

61 GTAGTGAATAGAGTTAGGCAGGGATATTTCACCATTATCGTTTCAGACCCACCTCCCAATC 120

2527 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCT

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FEATURES

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LVBSPTVLESGARE
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LLQYWSQELKNSAVSLLNATAIAVABGTDRVIEVVQGAXRAIRHIPRRIRQGLERILL
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FTDNAKTIIVQLNQSVEINCTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHCNIS
RAKMNYTLKQIDSKLREQFGNNKTIIPKQSSGGDPEIVTHSFNCGGEFFYCNSTQLFN
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6404...7733
700te="tat, rev, nef subgenomic mRNA intron 2"
7420...5621...5652
70ote="tat, rev, nef subgenomic mRNA intron 2"
70ote="vpu protein"
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ilarity 100.0%; Pred. No. 3.7e-28;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                    join(5328. .5403,7734. .8008)
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/note="envelope polyprotein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="rev protein,
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                                                                                                                    <5189. .5403
/note="tat protein,
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/note="rev protein"
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/note="tat protein"
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/note="nef p:
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BENDYNTPVPRIKKKOSTKWRLVDFRELUKRTODFREVQLGIPPHAGLTHEKKEVTVL
DVGDAYFSVPLDEDFRYTARFI ISINNETPGIRVQYWLLPGGWKGSPAIFOSSMTKI
LEPPKKQNPDIVIYQYMDDLYVGSDLEIGQHRTKIEELRRGLLRWGLTTPDKKHQKER
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VILVANHVASGYIBAEVIPAEDGQETAYFLIKLAGRWPVKTIHTDNGSNFTSATVKAA
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KLBEDQNKSKKAQQAAADTGHSSQVSQNYPIYQNIQSQMWHQAISPRTLNAWYKVVB
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KALGPAALTIMQRGARPROQROVKKYVLARAMSOYTNYTATIMQRGARPROQROVYKC
FNUCKEGHTARNCRAPRKKGGWKCGKEGHQMCDCTERQANFLGKIIMSSYKGRPONFLO
SRPEPTAPPFLQSRPEPTAPPEESFRSCVETTTPPQKQBPIDKELYPLTSLRSLRGND
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VWGRDNNSPSEAGADRQGTVSFNFPQITLWQRPLVTIKIGGQLKEALLDTGADDTVLE
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RGTKALTEVIPLTEEAELELAENREILKEPVHGVYYDPSKDLIAEIQKQGQGGWTYQI
YQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWE
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VTNKGRQKVVPLTNTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAQPDKSES
ELVNQIIEQLIKKEKVYLAWVPAHKGIGGNEQVDKLVSAGIRKILFLDGIDKAQDEHE
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66. .5135
112. .1650
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                                                                                                                                                                                                                                                                                                                                                                           /note="gag polyprotein precursor"
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db xref="GI:326389"
  b have been detected.
Location/Qualifiers
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and 1.8 kb have
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PAT 22-FEB-2001

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Tratrcaraardaragaaggcriggraggrrraagaaragritriggrigiagrific 7689
           61 GIAGIGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCCACCTCCCAATC 120
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Polymucleotide amplification method
Polymucleotide anplification method
Polymucleotide and 10.7661-A 3 01-FEB-2001;
Gen-Probe Incorporated (US)
1. .8933
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                                                                                                                                                                                                                                                    Human immunodeficiency virus
Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
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Patent: WO 0107661-A 4 01-FEB-2001;
Gen-Probe Incorporated (US)
Location/Qualifiers
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Sequence 4 from Patent WO0107661.
AX078308
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Sequence 3 from Patent WO0107661.
AX078307
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Best Local Similarity
Matches 129; Conserv
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TITLE
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AX078307
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               7689 GTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 7748
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100.0%; Pred. No. 3.7e-28;
ive 0; Mismatches 0;
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100.0%; Score 129; DB 6;
Best Local Similarity 100.0%; Pred. No. 3.7e-28;
Matches 129; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                  Chang, N.T., Gallo, R.C. and Wong-Staal, F. Cloning and expression of HTLV-III DNA Patent: US 6001977-A 4 14-DEC-1999; Location/Qualifiers
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Chang,N.T., Gallo,R.C. and Wong-Staal,F.
Detection of HIV-1 DNA
Patent: US 6610476-A 4 26-AUG-2003;
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                                                                                                                                                               DNA
                                                                                                                                                       8933 bp
Sequence 4 from patent US 6001977.
AR094659.1 GI:10021783
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Sequence 4 from patent US 6610476.
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/organism="unknown"
/mol_type="genomic DNA"
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                                                         CCGAGGGGA 129
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PAT 22-FEB-2001

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases I to 9748)

Nanshii, T.C.
CLONING AND DEVELOPPING OF HTLV-III DNA.

LA Patent: JP 1987026300-A 1 04-FEB-1987;
SRITOXOO INC
OS human(homo sapiens)
PN 1987026500-A/1
PN 1987026500-A/1
PP 11-OCT-1985 UP 1985226658
PR 10-OCT-1984 US 84 659339, 23-JAN-1985 US 85 693866 PI
PR 10-OCT-1984 US 84 659339, 23-JAN-1985 US 85 CO7KIS/12, CI2NS/00,
PC CIZNIS/00, A61K33/21, A61K39/395, CO7H21/04, CO7KIS/12, CI2NS/00,
PC CIZP21/OO, CI2D21/OB, G01N33/577;
CC Strandedness: Double;
CC topology: Linear;
CC typothetical: No;
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579..786
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1182..>185
/product='gag p24'/gene='gag p24'/gene='gag p24'/saga p22'/saga p2'/saga p2'/sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product='gag pl5 peptide'
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2082. 5126
/grocduct='pol peptide'
/gene='pol'
5041. 5649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5650. .6233
6234. .8822
/product='env-lor peptide'
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/organism="Homo sapiens"
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Location/Qualifiers
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/mol type="unassigned RNA"
/db xref="taxon:32630"
/note="Sequence of the IAC-Bscr pseudo target"
4140. .4159
/note="Mutated positions: 4140-42, 4145-47, 4152, 4156-57, 4159"
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4135. .4155
/note="Mutated positions: 4135, 4140-1, 4145, 4150,
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E01099.1 GT:2169358
JP 1987026300-A/1.
Homo sapiens (human)
                                                                                                                 Query Match
Best Local Similarity 100.0%; Score 129; DB 6;
Best Local Similarity 100.0%; Pred. No. 3.7e-28;
Matches 129; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.7e-28;
tive 0; Mismatches 0;
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Polynuclectide amplification method
Polynuclectide amplification method
Batent: WO 0107661-A 9 01-FEB-2001,
Gen-Probe Incorporated (US)
Location/Qualifiers
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                                                4152-3, 4155"
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synthetic construct
artificial sequences.
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Matches 129; Conservative
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 14 E01099

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8363 GTAGTGAATAGAGTTAGGCAGGGATATCACCATTATCGTTTCAGACCCACCTCCCAATC 8422
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                                                                                                                                                                                                                           5040 .5648
/note="SOR short open reading frame pot. vestigial env
                                                                                                                                                                                                                                                                                                     6323. .8824
/note="unnamed protein product; envelope glycoprotein"
                                    /note="pol precursor polypeptides put. protease at 5'
terminus reverse transcriptase put. endonuclease at 3'
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7787. 8821
7787. 8821
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7787. 9821
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700te="poly purine stretch"
9115. 9567
70te="long terminal repeat"
9115. 9567
70te="lug region"
9568. 9665
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100.0%; Pred. No. 3.7e-28;
tive 0; Mismatches 0;
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/note="polyadenylation signal"
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db_xref="G1:61574"
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9747. .9748
/note="inverted repeat"
                                                                                                                                                                                                  note="direct repeat"
                                                                                                                2128, .2163
/note="direct repeat"
2164. .2176
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                                                                                       terminus"
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Matches 129; Conservative
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/ codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mucsing,M.A., Smith,D.H., Cabradilla,C.D., Benton,C.V., Lasky,L.A. and Capon,D.J.
Nucleic acid structure and expression of the human
                                                                                                                                                                                                           lentivirus group.

1 (bases 1 to 9748)

Wong-Staal, F., Gallo, R.C., Chang, N.T., Ghrayeb, J., Papas, T.S.,

Lautenberger, J.A., Pearson, M.L., Petteway, S.R.Jr., Ivanoff, L.,

Bauneister, K., Whitehorn, E.A., Rafalski, J.A., Doran, E.R.,

Josephs, S.J., Starcich, B., Livak, K.J., Patarca, R., Haseltine, W.A.

and Rather, L.
                      X01762.1 GI:61569
acquired immune deficiency Byndrome; direct repeat; endonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="gag p24 and gag p15 for major capsid protein and
for put. retroviral nucleic acid binding protein
(NBP) (ref.2) (boundaries not defined)"
                                                                                                                                                                                       Viruses, Retroid viruses, Retroviridae, Lentivirus, Primate
                                                                            glycoprotein; inverted repeat; protease; provirus; reverse transcriptase; terminal repeat.
                                                                                                                                                                                                                                                                                                                                                                                 Complete nucleotide sequence of the AIDS virus, HTLV-III
Nature 313 (6000), 277-284 (1985)
851111123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .9748
/organism="Human immunodeficiency virus 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 635. .653 /note="tRNA binding site (tRNA-Lys)"
                                                                                                                                 Human immunodeficiency virus 1 (HIV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="long terminal repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIDS/lymphadenopathy retrovirus
Nature 313 (6002), 450-458 (1985)
85111157
2982104
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/note="inverted repeat"
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2031. .2065
/note="direct repeat"
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/product="gag p17"
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/note="R region"
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Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

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Minimum I Maximum I

Database

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CD850313 DHOAC38ZA
CD230347 SS1 43 D0
CD220247 CCCT_66_C
CG172989 PUFPC_46FD
CA8879214 mw85406.5
AA782068 a147b12.8
AA392668 a047b12.8
AA782068 a147b12.8
AA782068 a147b12.8
AA78225 C00435-F
AW788257 C01016-F
AW78825 AGENCOURT
CG11974 ZMMBBD026
BW906828 AGENCOURT
AZ245786 RPCT-23-7
AW783087 UF69D05.Y
BF035293 601457184
C69365 C69365 YUJJ
BW200729 BW200729
AG175005 PWA00729
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AG175005 PWA00729
AG175005 PWA00729
AG175005 PWA00729
AG175005 PWA00729
BZ434193 BOWRE91TR
BF182326 G018044076
BK2474051 BOWKC31F
AW855648 GGG1447F
AA87265 AG63401.8
AA865648 GGS461.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB03662.1 GI:6854195
BEST.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butherra; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases I to 317)
Mang.Y.L., Saigoh, K., Osaka, H., Yamanishi, T., Suh, J.G.,
Kiyoswa, H., Sakai, Y., Wakana, S. and Wada, K.
YACAG-Based physical and transcript mapping around the gracile
axonal dystrophy (gad) locus identifies uchli, pmx2b, atp3a2, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Degenerative Neurological Diseases
National Institute of Neuroscience, NCNP
4-1-1, Ogawahigashi, Kodaira, Tokyo 187-8502, Japan
Email: wada@ncnp.go.jp
RT-PCR primer based on the sequence that isolated from mouse BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                              CG172989
AA8792468
AA922668
BA986731
AA788423
AM788422
AW78842078
AW789257
AW789296
CG411974
BW206296
CG411974
BW206296
CG411974
BW206296
CG315398
AW763087
BW206729
AW763087
CC69365
BW206729
AW763087
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CC285081
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Genomics 66 (3), 333-336 (2000)
20334630
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10873389
                                      RESULT 1
AB036462/c
LOCUS
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 AB036462 AB036462
BH886550 LB00861a.
CG687892 ZMMBBC016
CC714059 OGUBX71TV
                                                               March 11, 2004, 19:37:35; Search time 1731.47 Seconds (without alignments) 1552.207 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                             1 atgagagtgaaggagaaata......tgttgatgatctgtagtgct
                                                                                                                                                                                                     55026578
      GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                               27513289 segs, 14931090276 residues
                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                            nucleic search, using sw model
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us-10-003-035-74.rst

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Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays subsp. mays (maize)

Zea mays subsp. mays

Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Zea anticoideae; Andropogoneae; Zea.

(Dases 1 to 809)

Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,

Zedovetz,V., Fuks,G., Yu.Y., Wing,R. and Messing,J.

Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                         266 ATGAGAGTAAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACATG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      575 TGAGTCTGCATGAGAACATCTGCACTATTGTCATTGGAGGTGGTGGTGGTGGAGGCAACTGC 634
                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sub_species="mays"
/db_xref="taxon:4578"
/db_xref="zawmseol65122"
/dlone="zawmseol65122"
/lab_host="ze_coli_bH108"
/clone_lib="Zawmsec_(EcoRI)"
/note="Vector: pTaRBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                       CG697892
ZMMBBC0165L22r ZMMBBC (ECORI) Zea mayB subsp. mays genomic clone
ZMMBBC0165L22 3', genomic survey sequence.
                                                                                                                                                               1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG
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                                                                          Length 527;
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                                                                                                                     Indels
                                                                      198.2%; Score 88.4; DB 28; 198.19; Pred. No. 4.7e-14; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                               206 CICCTIGGGAIGITGAIGATCIGIAGIGCT 177
                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 400.
                                                                                                                                                                                                                                                     61 CTCCTTGGGATGTTGATGATCTGTAGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG687892.1 GI:37585282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .809
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Class: BAC ends
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tes 89; Conserv
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Best Local Similarity
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clones (437N8,538024,Research Genetics) using exon trapping method.
Location/Qualifiers
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/clone lib="Leishmania major Friedlin BAC Library"
/clone="Vector: pCG270; Site 1: HindIII; Genomic DNA from
Leishmania major Friedlin in agarose blocks was partially
digested with HindIII, size selected, and ligated with
HindIII-digested pCG270 vector DNA, 10368 clones were
picked and arrayed in 384 and 96 will plates. Library
construction and arraying was carried out by ResGen
Corporation and clones and filters are available from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCCACCATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 ATGAGAGTGAAGGAGAATATCAGCACTTGTGGGGGGTGGGGGTGGAGGTGGGGCTCCATG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                527 bp DNA linear GSS 07-AUG-200 BAC Library Leishmania major Friedlin BAC Library Leishmania major genomic clone LB00861a, genomic survey sequence.
                                                                                                                                                                                                  /sex="male"
/tissue type="brain,liver,kidney,lung,heart,spleen"
/cell_line="GJ7 embryonic stem cell line"
/dev_stage="adult"
/clone_lib="Mus musculus GJ7 brain, liver, kidney, lung,heart, spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
1 (bases Lo 527)
Myler,P.J., Vogt,C., Munden,H., Robertson,L., Sisk,E.,
Fazelinia,G., Aggarwal,G., Nelson,S., Seyler,A., Worthey,E.,
Stuart,K. and Ragland,M.
Leishmania major Friedlin BAC End Sequences
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                  Score 90; DB 9; Length 317; Pred. No. 1.4e-14;
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Contact: Myler PJ
Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109-1651, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Leishmania major"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCTTGGGATGTTGATGATCTGTAGTGCT 52
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="129/Sv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="Friedlin"
                                                                                                                                   /db_xref="taxon:10090"
/map="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:5664"
clone="LB00861a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mylerpjæsbri.org
Seg primer: SP6
Class: BAC ends.
Location/Qualifiers
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                                                                                                                                                                               clone="13-3"
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Fax: 206 284-0313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leishmania major
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Best Local Similarity
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/mol_type="mRNA"
/cultivar="psc8"
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Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD230371.1 GI:30973805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                         53; Conservative
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OGUBX71TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0404K22, genomic survey sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
asterida; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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                                                                                                                                                                                                      1. (bases 1 to 925)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGUBX71TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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/clone="zwmBMa0404x22"
/clone="b=zm_0.7.i.5_xB"
/note="Vector: pBGSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helianthus annuus (common sunflower)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/mol type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 TCCTTGGGATGTTGATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD850313
CD850313.1 GI:32534135
                                                                              CC714059.1 GI:32118835
                                                                                                                                                                                                                                                                                                                                       Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: TF
Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                            Tel: 301-838-5843
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicodieae; Andropogoneae; Sorghum.

E 1 (bases 1 to 454)

Cordonnier-Pratt, M. M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Lidang, C., Sun, F., Sullivan, R., Shah, M., Summer, E.J., An Est database from Sorghum: salt-stressed seedlings

Unpublished (2003)

Unpublished (2003)

Unpublished (2003)

Contact: Cordonnier-Pratt, MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS1_43_D04.b1_A012_Salt-stressed seedlings Sorghum bicolor cDNA clone Ss1_43_D04_A012_3', mRNA sequence.
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Seq primer: Sug3 (CGACTGCAGCTCGAGCACA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).

Location/Qualifiers
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/cultivar="153620c"
/db_xref="txxxon:4558"
/clone="851 43 D04 A012"
/lab_host="DH10B-TI phage-resistant E. coli"
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60.9%; Pred. No. 99;
iive 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                                                                                                                                                              organism="Helianthus annuus"
                                                                                                                                                                                                                                                                                             /db_xxef="tâxon:4232"
/clone="HaDevR238A11"
/tissue_type="terminal bud"
/clone_lib="HaDevR2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CICCTIGGGAIGTIGAIGAICTGTAGT 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Sorghum.

E 1 (bases 1 to 51s)

Cordonnier-Pratt, M. M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Rathore, K., Ratman, A. and Pratt, L.H.

An EST database from Sorghum: callus culture and cell suspension Unpublished (2003)

Coher ESTS: CCC1 66 (O6.91 A007)

Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bicinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Fax: 706 583 0210
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/cultivar="RTx430"

/db_xxef="taxon:4558"

/clone="CCC1_66_C06_A007"

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/clone_lib="Callus culture/cell suspension"

/note="Vector: pME188-FL3; Site_1: XhoI; Site_2: XhoI; The
                                    2: XhoI; The
                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCC1 66 C06.b1 A007 Callus culture/Call suspension Sorghum bicolor CDNA clone CCC1_66_C06_A007 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mmpraticage edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
Library constructed by Dr. Miversity of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University,
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
are presented as their reverse complement and have been trimmed to
exclude polyA.

Seq primer: Sug3 (CGACCTGCAGCACAA)
/clone_lib="Salt-stressed seedlings"
//note="Vector: pWE18S-FL3; Site_1: XhoI; Site_2: XhoI; The library was prepared from polyA+ RNA from 9-day-old seedlings grown in hydroponic culture. Seedlings were transferred to a 150 mM NaCl solution and harvested at 3, 6, 12 and 24 hr following transfer. Roots and leaves were pooled from all time points and RNA isolated.
Double-stranded cDNA was cloned unidirectionally into different DrailI sites of the pME18S-FL3 vector (5-prime DrailI site is CACTGTGTG, 3-prime DrailI site is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 AGAGGITGIGGAGAIGCIGGIGGAGAITITGCAIGGGGGCCAITIGGAIGIAGAIGIITI 38
                                                                                                                                                                                                                                                                                                                                                                                                                               23 AGCACTIGIGGAGAIGGAGAIGGAGAIGGGCACCAIGCICCIIGGGAIGIIGAIGAICI
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                                                                                                                                                                                                                                                                                                                              35.6%; Score 32; DB 14; Length 45 68.8%; Pred. No. 1.4e+02; ive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Sorghum bicolor"
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Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD220247.1 GI:30963681
                                                                                                                                                                                                                                                                                                                                                                                  44; Conservative
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 44; Conserv
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LOCUS
DEFINITION
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AUTHORS
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           library was prepared from a mixture of polyA+ RNA from callus culture tissue and cells in suspension culture. Double-stranded cDNA was cloned unidirectionally into different DrallI sites of the pME188-FL3 vector (5-prime DralII site is CACTOTGTG, 3-prime DralII site is CACTOTGTG.
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/clone lb="ZM_06_1.0.KB"
/note="Vector: pCR4_T0F0; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGGAGATGGGGCACCATGCTCCTTG 67
                                                                                                                                                                                                                                                                 23 AGCACTIGIGGAGAIGGGGGIGGAGAIGGGGCCACCAIGCICCTIGGGAIGTIGAIGAICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 rearccaraagriccrecarrerresascrassesassissesassascriscresita
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                          .,
                                                                                                                                                                            Length 515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                        35.6%; Score 32; DB 14; Length 51 68.8%; Pred. No. 1.5e+02; ive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB 29; Length 94
Pred. No. 3.6e+02;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .940
/organism="Zea mays"
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Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 GGATGTTGATGATCTGTAG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG172989.1 GI:34063787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2003)
Other_GSSs: PUFPC46TB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.0%;
Matches 49; Conservative 0
                                                                                                                                                                        Query Match
Best Local Similarity 68.83
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                    83 GTAG 86
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LOCUS CA485128/c

ACCESSION

VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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Contract: Rocard Stratablerg, Ph.D.

Contract: Rocard Stratablerg, Ph.D.

Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,

Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnli.gov/bbrp/image/image.html

Seq primer: -40ml3 fwd. Ef from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA782068 274 bp mRNA linear EST 31-DEC-1998 al47bl2.81 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 1360127 3' similar to contains element MER28 repetitive element ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
/clone lib="NCI CGAP Priz"
/clone lib="NCI CGAP Priz"
/note="Vector: pAMP10, mRNA made from metastatic prostate
lesion of the bone, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
werage insert size 600 bp. Library made by D. Krizman,
NH."
                                                                                                                                                                                                                              Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 274)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                    1 (bases 1 to 225)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
nw85d06.sl NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1253387 similar to contains element MER28 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGAGAGTGAAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 AAGAGGAGGAAGAACTGCCAGAAGATGATGAGGAAGAGGAGGAGGAGGAGGAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="metastatic prostate bone lesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.6%; Score 30.2; DB 9; ilarity 60.2%; Pred. No. 3.4e+02; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 ATGATGATGATGATGATGTG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
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                                                                                                               AA879214.1 GI:2988179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
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Les 50; Conserv
                                                            sequence.
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/dav_stage="Meiotic stages pre-meiosis-metaphase I"
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/clone="bector: pSPORTI; Site 1: Sall; Site 2: Not!; Plants
/clone="Vector: pSPORTI; Site 1: Sall; Site 2: Not!; Plants
were grown in a glasshouse. Anther meiotic stage was
determined by removing anthers from individual primary
florets. One anther was sacrificed for microscopic
staging, and if determined to be between (and including)
meiotic stages pre-meiosis and metaphase I, the remaining
two anthers were collected and pooled for library
construction. The tissue, total RNA, and poly(A) RNA were
prepared, cDNA synthesised, and directionally ligated into
pSPORTI by Tim Sutton in the P Langridge Lab at the
Department of Plant Science, University of Adelaide, Waite
Campus Australia. Average insert size 1:SKD. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Fat: 5105595713
                                                                              CA485128 634 bp mRNA linear EST 14-NOV-2002 WHE4314_G11_M222S Wheat meiotic anther cDNA library Triticum aestivum cDNA clone WHE4314_G11_M22, mRNA sequence.
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                                                                                                                                                                                                                                                                                             Entricour accessions Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

I (basea: Triticeae; Triticum.

Anderson, O. D., Chao, S., Crossman, C., Langridge, P., Lazo, G.R., Pham, J., Rausch, C.J., Sutton, T., Woo, J. and Wilson, C.

The structure and function of the expressed portion of the wheat genomes - Meiotic anther cDNA library
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Pred. No. 3.9e+02;
0; Mismatches 34; Indels 0;
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quality sequence with phred score less than 20
Seq primer: SK primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
                                                                                                                                                                                                                                                Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 GTCCTTGGGATGATGAAGAAGGGTA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: oandersn@pw.usda.gov
                                                                                                                                                                                          CA485128.1 GI:24979133
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Query Match Best Local S: Matches 51,

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RESULT 10 AA879214/c LOCUS

us-10-003-035-74.rst

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CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: NWW-bio.llnl.gov/bbrp/image/image.html Insert Length: 1155 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="pooled germ cell tumors"
/lab host="Dellog"
/lab host="Thilbs"
/clone_lib="NCI_CGAP_GC4"
/note="Vector: pT713D-pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo (dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo.
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MR1-HT1183-040101-002-a06 HT1183 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1571882"
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Laboratory of Cancer Genetics
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Email: asimpson@ludwig.org.br
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            Smmert-Buck, M.D., Ph.D.
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                                                                Email: cgapbs-remail.nib.gy, constant of the partial constant of the paration of the partial of the paration of the partial constant of the paration of the paration of the paration of the properties of the paraty Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/Link at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 176.2 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="parathyroid tumor"
/dev_stage="adult"
/dev_stage="adult"
/dab_host="DHDB (ampicillin resistant)"
/clone_lib="Soares parathyroid tumor_NbHPA"
/clone_logan: parathyroid gland, Vector: pT7T3D
/hote="Corgan: parathyroid gland, Vector: pT7T3D
/hote="Corgan: parathyroid gland, Vector: pT7T3D
/site_2: Eco RI; lst strand cDNA was primed with a Not I -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 AAGAGGAGGAAGAACTGCCAGAAGATGATGAGGAAGAAGAGGAGGAGGAGGAAGATG 150
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(Dases 1 to 294)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGGTGGAGATGGGGCACCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Homo sapiens"
                                            Ph.D.
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db_xref="taxon:9606"
clone="1360127"
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                                            Contact: Robert Strausberg,
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24 GCACTIGIGGAGAIGGGGGIGGAGAIGGGGCACCAIGCICCTIGGGAIGII
                                                      33.6%; Score 30.2; DB 10; 74.5%; Pred. No. 4.2e+02; iive 0; Mismatches 13;
                                                                                                 Conservative
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Fax: 45 3327 4766
Email: Bwr@crc.dk
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                                                                                                                                                                                                     /organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="txxxon:9606"

/dw_xref="txxon:9606"

/dw_xref="Adult"

/clone_lib="HT1183"

/clone_lib="HT1183"

/note="Organ: head neck; Vector: puc18; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORBERES PCR (U.S. Letters Patent application:
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR1&t2=MR1-HT1183-04010-002-a06&t53=2001-01-04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 301.
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Blumeria graminis f. sp. hordei
Eukaryota; Fungi; Ascomyota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
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Department of Yeast Genetics
Carlaberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 4766
Fax: 45 3327 4766
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/lab_host="Hordeum vulgare"
/clone_lib="Lambda Zap, Stratagene"
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/db_xref="taxon:62688"
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AW789257 01-MAY-2001 C01016-F Lambda Zap, Stratagene Blumeria graminis f. sp. hordei cDNA clone C01016 similar to adenylyl cyclase-associated protein 2,
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Blumeria graminis f. sp. hordei
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
I (bases I to 400)
Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and
289 GCCCTGGTGGGGGGGGGGGGGGGGGCACAAGGTGCCTTGGATTGTT 239
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Department of Yeast Genetics
Carlsberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell type="conidia"
/lab host="Hordeum vulgare"
/clone lib="Lambda Zap, Stratagene"
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/db_xref="taxon:62688"
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Job time : 1739.8 secs
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POLYA=No.
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                                                                                                                                                                                                                                mRNA sequence.
AW789257
AW789257.1 GI:13900854
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Dase : GenEmbl:*

1: gb ba:*
2: gb_ntg:*
3: gb_nn:*
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5: gb_ov:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		φo			SUMMARIES		
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	1	100.0	108	14	AV289013	AV289013 HTV-1 CL	
1 72		100.0	108	1 -1	HIVLAVAE	Human im	
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27			2945	o vo	AR365081	AR365081 Sequence	
28		-	8932	14	HIVBH102	M15654 Human immun	
30,8		0.001	8933	9 4	AR094659	AR094659 Sequence	
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32		100.0	8933	φ	AX078308		
33		-	8933	v v	AX078313	AX078313 Sequence	
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37		100.0	9748		REHTLV3	Ä	
2 C			0472	٥ ٢	TO/DAS HIVDVOO	K02083 Muman immin	
40			126	4	HIVCLAAA	Human	
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42 10	06.4	œ o	108	4.	HIVLAIAC	M64196 Human immun	
4			108		HIVLAIAH	Human	
1 -	4.9		108	14	HIVLAIAJ	Human	
					ALIGNMENTS		
RESULT 1							
AIZBYOLS	AY28	AY289013			108 bp DN	VRL	
DEFINITION	HIV-1 parti	1 clone ial cds.	e BAL#21 8.		from USA envelope glycoprotein	rotein (env) gene,	
ACCESSION VERSION	AY289	9013	GI:32	26404)45		
KEYWORDS							
SOURCE ORGANISM	Human	Human immu Human immu Vinsee: P	Human immunodeiiciency Human immunodeficiency Vinises: Betroid vinis	iency v	Virus 1 (ALV-1) Virus 1 Se: Detroxitidae:	Lentiviries Orimate	
	lent	entivirus	group.		100000000000000000000000000000000000000		
AUTHORS	Hosh	1 (bases Hoshino Y.		. B.	ochford.G.,	C.S., Hoshino,S.,	
	Кима	Kuwabara, K.	., Ching, E.,	E E	Raju, B., Gol	d,J.A., Borkowsky, W., Rom, W.N.,	

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'organism="Human immunodeficiency virus 1"
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                 The Innate Immune Response to Tuberculosis Alters CXCR4 (CD184) and Beta Chemokine Expression Enhancing HIV-1 X4 Strain Entry into
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                                                             Unpublished

(bases 1 to 108)

Hoshino, Y., Tse, D.B., Rochford, G., Prabhakar, S., Hoshino, S.,
Kuwabara, K., Ching, E., Raju, B., Gold, J.A., Borkowsky, W., Rom, W.N.,
Weiden, M. and Pine, R.

Direct Submission
Submitted (01-May-2003) Medicine, New York University Medical
Center, 462 First Avenue NB 8E38, New York, NY 10016, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                      "mol type="genomic DNA"
/isolation source="patient co-infected with tuberculosis;
trom bronchoalveolar lavage fluid"
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91240282
2035026
Original source text: Human immunodeficiency virus type 1 (HIV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in (sites) ... Vartanian, J.-P., Henry, M., Chenciner, N., Chain-Hobson, S., Vartanian, J.-P., Henry, M., Chenciner, N., Cheynier, R., Delassus, S., Martins, L.P., Sala, M., Nugeyre, M.-T., Guetard, D., Klatzmann, D., Gluckman, J.-C., Rozenbaum, W., Barre-Sinoussi, F. and Montagnier, L.
LAV revisited: origins of the early HIV-1 isolates from Institut
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Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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                                                                                                                                                                                                                                                         organism="Human immunodeficiency virus 1"
                                                                                                                                                                                                                                                                                                                                                                 /country="USA"
/note="anti-CD14 antibody captured"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="envelope glycoprotein"
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                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:11676"
/clone="BAL#21"
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Location/Qualifiers
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/gene="env"
/note="V3 region"
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Weiden, M. and Pine, R.
                                                  Alveolar Macrophages
                                                                                                                                                                                                                                                                                                                                                                                                                       "gene="env"
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Matches 108; Conserv
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Human immunodeficiency virus type 1 (HIV-1) envelope gene V3
region, partial cds.
                                                                                                                                                                      /produčt="envelope protein"
Protein id="AAA44159.1"
/db_xref="G1:37908"
/translation="CTRPNNNTRKSIRIQRGPGRAFVTIGKIGNWRQAHC"
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Human immunodeficiency virus 1 (HIV-1)
Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroinidae; Lentivirus; Primate
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/organism="Human immunodeficiency virus 1"
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llarity 100.0%; Pred. No. 4.5e-20;
Conservative 0; Mismatches 0;
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Pred. No. 4.5e-20;
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Science 249 (4971), 932-935 (1990).
90364416
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/gene="env"
                                                                             gene="env"
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Matches 108; Conserv
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Qy 1 TGTACAAGACCAACAACAATACAAGAAAAAGTATCCGTATCCAGAGACGACCAGGAGA 60 TGTACAAGACCCAACCAACAATACAAGAAAAGTATCCGTATCCGAGGAGACCAGGGAGA 60 Qy 61 GCATTTGTTACAATAGGAAAATATGAGAACAAGCAATTGT 108 Db 61 GCATTTGTTACAATAGGAAAATATGAGACAAGCACATTGT 108	108 bp 1132921 1132922 11329221 11329221 11329221 11329221 11329221 11329221 11329221 11329221 11329221 11329221 11329221 11329221 11329221 11329221 11329221 11329221 11329221 113292222222222	Best Local Similarity 100.0%; Pred. No. 4.5e-20; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TGTACAAGACCCAACAACAATACAAGAAAAGTATCCGTATCCAGAGAGACCACGGGAGA 60 Db 1 TGTACAGACCCAACAATACAAGAAAAAGTATCCGTATCCAGAGAGCACCAGGGAGA 60 Oy 61 GCATTTGTACAATAGGAAAAATATGAGAAATATGAGACAATTGT 108 Db 61 GCATTTGTACAATAGGAAAAATAGGAAATATGAGACAATTGT 108	Invol68 Inman immunodeficiency aggion, partial cds. 51584.1 GI:32329 Invelope-associated provelope-associated provelope-associated provelope-associated provelopes, Retroid viruses; Invological to 108) Roses, G.J., Langlois, J. Banduck, P., Holley, L., Banduck, P., Holley, L., Batthews, T.J., Banduck, P., Banduck, P., Banduck, P., Holley, L., Batthews, T.J., Banni, B. Stranger, G., C., Davide, J., Batthews, T.J., Banni, B. Rosa, G.J., Davide, J., Banduck, P., Holley, L., Batthews, T.J., Banni, B. Rosa, G.J., Melley, L., Banduck, P., Holley, L., Banni, B. Rosa, G.J., Weinhold, R. Rosa, G.J., Rosa, R.	Best Local Similarity 100.0%; Pred. No. 4.5e-20; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Direct Submission
Submitted (OB-DEC-1995) Hiroshi Ushijima, The University of Tokyo,
Submitted (OB-DEC-1995) Hiroshi Ushijima, The University of Tokyo,
Faculty of Medicine, Department of Maternal and Child Health; Hongo
7-3-1, Bunkyo-ku, Tokyo 113, Japan
(E-mail:ushijima@m.u-tokyo.ac.jp, Tel:+81-3-3812-2111(ex.3515),
Fax:+81-3-5802-2961)
On Jan 18, 1997 this sequence version replaced gi:1122714.
                                                                                                                                                                                                                     VRL 05-FEB-1999
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Kakizawa, J., Ushijima, H., Morishita, Y., Oka, S., Ikeda, Y. and
Muller, W.E.
                                                                                                                                                                                                                                                                                                                                                                                                                     Kakizawa, J., Ushijima, H., Morishita, Y., Oka, S., Ikeda, Y. and
Muller, W.E.
                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus 1 (HIV-1)
Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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/translation="CTRPNNVTRKSIRIQRGPGRAFVTIGKIGNMRQAH"
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/mol type="genomic RNA"
/isolate="No.5"
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ilarity 100.0%; Pred. No. 4.5e-20;
Conservative 0; Mismatches 0;
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/clone="A-1"
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<1. >105
/gene="env"
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Human immunodeficiency virus type 1 (HIV-1) envelope gene V3
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Conserved sequence and structural elements in the HIV-1 principal neutralizing determinant: further clarifications
                                                                                                                                                                                                                                                                                                                                                                                                lentivirus group.

(bases 1 to 108)
LaRosa,G.J., Davide,J.P., Weinhold,K., Waterbury,J.A., Profy,A.T.,
Lewis,J.A., Langlois,A.J., Dreesman,G.R., Boswell,R.N.,
Shadduck,P., Holley,L.H., Karplus,M., Bolognesi,D.P.,
Grathews, T.J., Emini,B.A. and Putney,S.D.
Conserved sequence and structural elements in the HIV-1 principal
neutralizing determinant
Science 249 (4971), 932-935 (1990)
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  TGTACAAGACCCAACAACAATACAAGAAAAAGTATCCGTATCCAGGAGGACCAGGGAGA
                                 TGTACAAGACCCAACAACAATACAAGAAAAAGTATCCGTATCCAGAGAGGACCAGGGAGA
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/product="envelope protein"
/protein_id="AAA45271.1"
/db_xref="G1:32924"
/translation="CTRPNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHC"
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                                                                                                 organism="Human immunodeficiency virus 1"
                                                                            GCATTTGTTACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT
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envelope-associated protein.
Human immunodeficiency virus I (HIV-1)
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/db_xref="taxon:11676"
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Nature 313 (6002), 450-458 (1985)
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Wain-Hobson,S.
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                                                                                                                                                                                        Nara, P.L., Smit, L., Dunlop, N., Hatch, W., Merges, M., Waters, D., Kellhar, J., Gallo, R.C., Fischinger, P.J. and Goudamit, J.
Emergence of viruses resistant to neutralization by W3-specific antibodies in experimental human immunodeficiency virus type 1 IIIB infection of champanases
T. Mirol, 64 (8), 3779-3791 (1990)
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                     VRL 02-AUG-1993
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/protein_id="AAA44281.1"
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Muceing, M., Smith, D.H., Cabradilla, C.D., Benton, C.V., Lasky, L.A.
and Capon, D.J.
Nucleic acid structure and expression of the human
AIDS/lymphadenopathy retrovirus
                                                                                                                                                                                                                                                                                                              source text: Human immunodeficiency virus type 1 (strain viral RNA, clone C3. Location/Qualifiers
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Human immunodeficiency virus 1 (HIV-1)
Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroid viruses; Primate
                      HIVC3AA linear VRL 02-A
Human immunodeficiency virus type 1 envelope gene V3 region,
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Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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1 (bases 1 to 276)
Wain-Hobson,S., Sonigo,P., Danos,O., Cole,S. and Alizon,M.
Nucleotide sequence of the AIDS virus, LAV
Cell 40 (1), 9-17 (1985)
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/codon_start=1
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/protein_id="aAC37917.1"
/db_xref="GI:1128994"
/translation="VVIRSANFTDNAKTIIVQLNQSVQINCTRPNNWTRKSIRIQRGP
GRAFVTIGKIGNMRQAHCNISRAKMNATLKQIASKLREQFGNNKTIVF"
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Lukashov,V.V. and Goudsmit,J.
Lucreasing genotypic and phenotypic selection from the original
genomic RNA populations of HIV-1 strains IAI and MN (NN) by
peripheral blood mononuclear cell culture, B-cell-line propagation
and T-cell-line adaptation
AIDS 9 (12), 1307-1311 (1995)
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Rusched, J.R., Putney, S.D., Javaherian, K., Farley, J., Grimaila, R., Iymn, D., Petro, J. and O'Keeffe, T.
Novel HIV proteins and o'Keeffe, T.
Novel HIV proteins and peptides useful in the diagnosis, prophylaxis or therapy of AIDS
Patent: EP 0306219-A2 7 08-MAR-1989;
Location/Qualifiers
Wain-Hobson, S., Vartanian, J.-P., Henry, M., Chenciner, N., Cheynier, R., Delassus, S., Martins, L.P., Sala, M., Nugeyre, M.-T., Guetard, D., Klatzmann, D., Gluckman, J.-C., Rozenbaum, W., Barre-Sinoussi, F. and Montagnier, L.
LAV revisited: origins of the early HIV-1 isolates from Institut
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1. .276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Human immunodeficiency virus 1"
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EP 0306219.
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*uo pp DNA linear VRL 12-OCT-1996
Human immunodeficiency virus type lisolate D22/448 envelope
glycoprotein gp120 (env) gene, c2v3 region, partial cds.
U40539
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nvsfvvgcthgirpvvstglllngslabebevvirsanftdnaktiivglngsveinctr
pnnntrksirigagpgrafvtigkignmrgahc"
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Quinones-Wateu, M.E.
Direct Submission
Submitted (13-NOV-1995) Miguel E. Quinones-Mateu, Centro de
Biologia Molecular 'Severo Ochoa', Universidad Autonoma de Madrid,
Cantoblanco, Madrid, 28049, Spain
On Oct 16, 1996 this sequence version replaced gi:1304535.
Location/Qualifiers
    Point mutant frequencies in the pol gene of human immunodeficiency virus type 1 are two- to threefold lower than those of env AIDS Res. Hum. Retroviruses 12 (12), 1117-1128 (1996)
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Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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1 (bases 1 to 405)

Quinones-Mateu,M.E., Holguin,A., Soriano,V. and Domingo,E. env gene diversity of HIV type 1 isolates from Spain AIDS Res. Hum. Retroviruses 12 (10), 955-957 (1996)
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Quinones-Mateu, M.E., Holguin, A., Dopazo, J., Najera, I. and
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                                                                                                                                                                                                                                                                                organism="Human immunodeficiency virus 1"
                                                                                                                                                                                                                                                                                                  /moi_type="genomic DNA"
/isolate="D22/+28"
/specific_host="Homo sapiens"
/db_xref="taxon:11676"
(cl] type="peripheral blood lymphocytes"
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protein id="AAC55849.1"
/db_xref="GI:1304536"
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Pred. No. 4.2e-20;
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/gene="env"
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Best Local Similarity 100.8
Matches 108; Conservative
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Rusche, J.R., Putney, S.D., Javaherian, K., Farley, J., Grimaila, R.,
Lynn, D., Petro, J. and O'Keeffe, T.
Novel HIV proteins and peptides useful in the diagnosis,
prophylaxis or therapy of AIDS
Patent: EP 0306219-A2 9 08-MAR-1989;
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Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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Quinones-Mateu,M.E., Holguin,A., Soriano,V. and Domingo,E.
env gene diversity of HIV type 1 isolates from Spain
AIDS Res. Hum. Retroviruses 12 (10), 955-957 (1996)
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Quinones-Mateu, M.E., Holguin, A., Dopazo, J., Najera, I. and
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100.0%; Pred. No. 4.3e-20;
iive 0; Mismatches 0; Indels
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                /organism≂"unknown"
/mol_type="unassigned DNA"
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Sequence 9 from Patent EP 0306219.
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Best Local Similarity 100.0%;
Matches 108; Conservative 0
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Matches 108; Conservative
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1. .288
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NVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSANFTDNAKTIIVQLNQSVEINCTR
PNNNTRKSIRIQRGPGRAFVTIGKIGNMRQAHC"
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                           3 (bases 1 to 405)
Quinones-Mateu, M.E.
Direct Submission
Submitted (13-NOV-1995) Miguel E. Quinones-Mateu, Centro de
Biologia Molecular 'Severo Ochoa', Universidad Autonoma de Madrid,
Cantoblanco, Madrid, 28049, Spain
On Oct 16, 1996 this sequence version replaced gi:1304537.
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Rusche, J.R., Putney, S.D., Javaherian, K., Farley, J., Grimaila, R.,
Lynn, D., Petro, J., and O'reaffe, T.
Lynn, D., Petro, J. and O'reaffe, T.
Lynn, D., Petro, J. and O'reaffe, T.
Lynn, D., Petro, J. A. 128
Rocant, FP 0206219-AZ 11 09-MAR-1989,
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                                                                                                                                                                              organism="Human immunodeficiency virus 1"
                                                                                                                                                                                 /proviral /moultype="genomic DNA" /isolate="D22/+48" /isolate="D22/+48" /db xref="taxon:11676" /cell type="peripheral blood lymphocytes" 1. 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                            product="envelope glycoprotein gp120"
protein id="AAC55850.1"
/db_xref="GI:1304538"
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105605 1 GI:590568
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                note="c2v3 region"
                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                gene="env"
                                                                                                                                                                                                                                                                                                                                                gene="env"
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97000986
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SOURCE
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FEATURES
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115 TGTACAAGACCCAACAACAATACAAGAAAAAGTATCCGTATCCAGAGAGGACCAGGGAGA 174
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Putney, S.D., Lynn, D., Javaherian, K., Mueller, wt. and farley, J.
Recombinant polypeptides and their uses, inclusing assay for aids
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100.0%; Score 108; DB 6; Length 536;
Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 108; Conservative 0; Mismatches 0; Indels (
                                             61 GCATTIGITACAATAGGAAAATAGGAAATATGAGACAAGCACATTGT
                                                                             GCATTTGTTACAATAGGAAAATAGGAAATATGGGAAAATATGGGACAAGCACATGT
                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent: EP 0255190-A2 5 03-FEB-1988;
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 5 from Patent EP 0255190.
105295
105295.1 GI:591127
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                                                                                                                                                                                                                                                                                                                                                            Unclassified.
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March 11, 2004, 18:51:27; Search time 304.156 Seconds (without alignments) 1801.765 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                       3373863 seqs, 2124099041 residues
                                                                                      nucleic search, using sw model
                                                                                                                                                                                                                                                                                                     IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 20000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	gp4	Add66326 HIV gp41	Adb87771 HIV-1 p17	Add66293 HIV p17 m	HIV	Add66299 HIV p24 m	DEN	Aag28095 Recombina	Adb87765 HIV-1 pl7	Add66287 HIV p17/2	Aan90531 Sequence		Add66267 HIV clone	Aan80949 HIV prote	3 HIV-	Add66275 HIV E m/E	Adb87752 HIV-1_BH1	Add66274 HIV E mde	Aat05127 HIV vīrus	Adb87751 HIV-1 BH1	Add66273 HIV E mde	Aan60128 Seguence	Adb87743 HIV-1 str
SUMMARIES		ID	ADB87802	ADD66326	ADB87771	ADD66293	ADB87777	ADD66299	AAQ03968	AAQ28095	ADB87765	ADD66287	AAN90531	ADB87745	ADD66267	AAN80949	ADB87753	ADD66275	ADB87752	ADD66274	AAT05127	ADB87751	ADD66273	AAN60128	ADB87743
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		Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparastic, protozoacide, cytostatic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against

New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor

Claim 24; Page 81; 156pp; English.

antigens

Add66265 HIV clone	Adb87750 HIV-1 BH1	Add66272 HIV Env m	Adb87781 HIV-1 mod	Add66303 Modified	Aah76385 Nucleotid	Aaf60548 IAC-Bscr		Aaf60542 Plasmid B	Aaq45921 HTLV-III		Aan60240 HTLV-III	Aaq45922 HTLV-III		Aaa97933 HIV-1 env	Aan90398 HIV-1 env	HI	Aaf56366 HIV gene.	Aav36264 Human imm	Adb87749 HIV-1 str	Add66271 HIV E_mde	Aaq33473 HD1(T7).
3 ADD66265	9 ADB87750	3 ADD66272	9 ADB87781	9 ADD66303	4 AAH76385	4 AAF60548	4 AAF60543	4 AAF60542	2 AAQ45921	2 AAQ45919	1 AAN60240	2 AAQ45922	5 AAS19260	3 AAA97933	1 AAN90398	5 AAH20891	4 AAF56366	2 AAV36264	9 ADB87749	9 ADD66271	2 AAQ33473
3157	3417 9	3417 9	3839	3839	8932 4	8933 4	8933 4	8933 4	9425	9425	9745 1	9749	9918	2148	2263 1	2562	2565 4	2730	2746	2746	2940
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.8	98.8	98.8	98.8	98.8	98.8	98.8	98.8
129	129	129	129	129	129	129	129	129	129	129	129	129	129	127.4	127.4	127.4	127.4	127.4	127.4	127.4	127.4
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

N Geneseq 29Jan04:*

Database

geneseqn1980s:* geneseqn1990s:* geneseqn2000s:*

geneseqn2001as:* geneseqn2001bs:* geneseqn2003as:* geneseqn2003cs:* geneseqn2004s:*

geneseqn2002s:*

adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial; antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine; pathogen; Ebola virus; hepatitis virus; tumour antigen; ds. Human immunodeficiency virus 1. BP gp41 transmembrane domain DNA. 02-JUN-2000; 2000US-00585599. 04-JUN-2001; 2001WO-US018238. 01-NOV-2001; 2001US-00003035. ADB87802 standard; DNA; 129 (first entry) WPI; 2003-182621/18. US2002155127-A1. (WANG/) WANG D. 04-DEC-2003 24-OCT-2002. ADB87802; Wang D; ADB87802

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced; infection; influenza; Ebola; Marburg; Arbovirus; hepatitis; respiratory syncytial virus; herpes simplex virus; human papilloma virus;
infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BH10 antigen construct described in the disclosure of the
                                                                                                                                                                                                                                                               GTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 120
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                                                                                                                                                                                                         TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTTAAGAATAGTTTTTGCTGTACTTTTCT
                                                                                                                                                              Gaps
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                                                                                                                                     Length 129;
                                                                                                                                                             Indels
                                                                                                        Sequence 129 BP; 34 A; 22 C; 31 G; 42 T; 0 U; 0 Other;
                                                                                                                                                1,1e-30;
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                                                                                                                                                              0; Mismatches
                                                                                                                                   100.0%; Score 129; 100.0%; Pred. No. 1
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04-JUN-2001; 2001WO-US018238.
01-NOV-2001; 2001US-00003035.
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                                                                                                                                                   Best Local Similarity 100.
Matches 129; Conservative
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                                                                                  invention.
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The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence

Example; SEQ ID NO 75; 185pp; English.

recombinant adenovirus.

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This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparasitic, protozoacide, cytostatic and useful as immunemodulatory activity. The recombinant adenoviruses are useful as carrier at a ganthogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, cotozoans, e.g. malaria. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immunactimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BHIO antigen construct described in the disclosure of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           new recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
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                                                                                                        Gaps
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                                                                   Length 129;
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                                Sequence 129 BP; 34 A; 22 C; 31 G; 42 T; 0 U; 0 Other;
                                                                   100.0%; Score 129; DB 9;
ilarity 100.0%; Pred. No. 1.1e-30;
Conservative 0; Mismatches 0;
is used in the exemplification of the invention.
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04-JUN-2001; 2001WO-US018238.
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                                                                                                                                                                                                                                                                                                 CCGAGGGGA 129
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                                                                                          Similarity
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                                                                                                                                                                                                       GTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced; infection; influenza; Ebola; Marburg; Arbovirus; hepatitis; respiratory syncytial virus; herpes simplex virus; human papilloma virus;
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                                                                                                                                                                                     GTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 120
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                                                              Length 615;
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                               Sequence 615 BP; 217 A; 101 C; 162 G; 135 T; 0 U; 0 Other;
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                                                            100.0%; Score 129; DB 9; 100.0%; Pred. No. 1.6e-30;
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                                                                                                                                                                                                                                                                                                                                                            ADD66293 standard; DNA; 615 BP.
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04-JUN-2001; 2001WO-US018238.
01-NOV-2001; 2001US-00003035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus
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                                                                            Best Local Similarity 100.
Matches 129; Conservative
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                                                         Query Match
Best Local Similarity
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 invention
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This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparasitic, protozoacide, cytostatic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also to useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BH10 antigen construct described in the disclosure of the
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                                                                                                                                                                                                                                                                                                                 544 GTAGTGATTAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC
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                                                   Indels
                                                                                                                    1 TIATICATAAIGATAGIAGGAGGCTIGGIAGGITTAAGAATAGTI
                       Pred. No. 1.6e-30;
Mismatches 0;
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100.08; 22
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2001WO-US018238
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04-JUN-2001;
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DB 9; Length 915;

100.0%; Score 129;

Query Match

100.0%; Score 129; DB 9; Length 615;

Query Match

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784 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCT 843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         against HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced; infection; influenza; Ebola; Marburg; Arbovirus; hepatitis; respiratory syncytial virus; herpes simplex virus; human papilloma virus;
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                                                          Indels
                        1.8e-30;
nes 0;
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Mismatches
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100.0%; Pic
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04-JUN-2001; 2001WO-US018238.
01-NOV-2001; 2001US-00003035.
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                               Conservative
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P-PSDB; ADD66302.
                    Similarity
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                                                129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence encodes ENV9, a recombinant peptide. ENV9 consists of about 54 amino acids from the N-terminal of a poliovirus sequence (pEXC), as well as those regions of HIV gpl20 and gp41 detailed above. ENV9 can be used to detect HIV antibodies. "False positive" results are minimised as it contains few non-critical antigens. It can also be used in a vaccine
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                        844 GTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                              pENV9 encoding a recombinant peptide with HIV antigenicity.
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0; Mismatches 0;
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Best Local Similarity 100.
Matches 129; Conservative
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TTATTCATAATGATAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCT

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adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial; antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine; pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.

Human immunodeficiency virus 1.

US2002155127-A1.

24-OCT-2002

01-NOV-2001; 2001US-00003035. 02-JUN-2000; 2000US-00585599. 04-JUN-2001; 2001WO-US018238.

HIV-1 p17/24 membrane form DNA SEQ ID 36.

(first entry)

04-DEC-2003

ADB87765;

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us-10-003-035-75.rng

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The plasmid pENV9 was constructed by ligating the BqlII/BamHI fragment (Int 7196-8053) of HIV clone lambda BH10 with the BglII/ BamHI vector fragment of pexc. The prod. was used to transform B. coli strain HB101 and MM294. The transformates produced a protein ENV9 contg. 349 amino acids from the N. terminal of the pollovirus sequence of pEXC, 46 amino acids from the N. terminal of the pollovirus sequence of pexc. 46 amino acids of the C. terminal of the peptide comprises the early detection antigen from gp120 and a highly reactive comprises the early detection antigen from gp120 and a highly reactive antigen from gp121 thus providing broad sensitivity to HIV antibodies. The sensitivity of the peptides permits the detection of HIV infection using secondare to larger antigence segments. The peptides have improved stability as compared to larger antigenic segments and contain fewer noncritical antigens which minimises the possibility of false positive results in detection of HIV infection. The peptides can also be used in vaccines protective against HIV. (Updated on 25-MAR-2003 to correct PP field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding a HIV antigen - comprising the C-terminal N-terminal of Gp41. for use in diagnosis and in
                                                                                                                                                                                                                                                                                                                                                                                Poliovirus; HIV; human immunodeficiency virus; AIDS; gp120; gp41; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 129; DB 2; Length 1026; 100.0%; Pred. No. 1.8e-30; Live 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1026 BP; 335 A; 178 C; 275 G; 238 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DUPO ) DU PONT DE NEMOURS & CO
                                        AAQ28095 standard; DNA; 1026 BP
                                                                                                                                                                                                                                                                                                            Recombinant DNA encoding ENV9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Fig 4; 12pp; English
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Best Local Similarity 100.0%;
Matches 129; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-00347004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87US-00010056
                                                                                                                                                                                                    (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence region of Gp120 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-307861/37.
P-PSDB; AAR26787.
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                                                                                                                                                                                            25-MAR-2003
12-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                        AAQ28095;
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AAQ28095
XX
XX
AAQ2
XX
AAQ2
XX
AAQ2
DT 12-F-M
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New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor

WPI; 2003-182621/18.

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(WANG/) WANG

Wang D;

Claim 30; Fig 50A; 156pp; English.

antigens

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This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparastic, protozoacide, cytostatic and immunomodulatory activity. The recombinant adenoviruses are useful as infection of a pathogenic antigen, e.g. HIV, Boola virus, hepatitis A, B, C, D or E or tumour antigens, e.g. HIV, Boola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-I strain BHIO antigen construct described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1237 GTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTTAAGAATAGTTTTTGCTGTACTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 1.9e-30;
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100.0%; Score 129; Dest Local Similarity 100.0%; Pred. No. 1.9
Matches 129; Conservative 0; Mismatches
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Best Local Similarity
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TIATICATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCT 879 GTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 120 GTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 939

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TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCT

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Gaps

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ADD66287 standard; DNA; 1308 BP.

RESULT 10 ADD66287 ID ADD66

RESULT 9 ADB87765 ID ADB87765 standard; DNA; 1308 BP.

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ADD66287;

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Fusion protein gene comprises the 0.9kbp gene fragment from Pvull site to BgIII site of HTLV-III gag gene, and 1.2kbp gene fragment from BgIII site to Xho I site of HTLV-III env gene. The HIV gag-env protein has the antigenicity of the gag and env proteins. It contains all the peptide domains of gag-p24 and env-gp41 that are esp. important antigens in a vaccine. The eukaryotic expression cell is pref. Saccharomyces cerevisiae. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1669 GTAGTGAATAGAGTTAGGCAGGATATTCACCATTATCGTTTCAGACCCACTCCCAATC 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                          Fusion protein of hiv gag-env - effective for an aids antibody assay reagent or vaccine - obtd. by expressing fused gene contg. fragment of coding from human immune virus gag gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial; antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine; pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1609 ITATTCATAAIGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 129; DB 1; Length 2237; Pred. No. 2.2e-30;
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                                                            HIV; fusion protein; gag; env; AIDS; vaccine; ss
                    Sequence encoding fusion protein of HIV gag-env.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                       Human T-cell lymphotropic virus III
                                                                                                                                                                                                                                                                                                                   (KAGA ) KAGAKU OYOBI KESSEI RYOHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB87745 standard; DNA; 2280 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim; Page ?; 12pp; Japanese.
                                                                                                                                                                                                                                    87JP-00336292
                                                                                                                                                                                                                                                                             87JP-00336292.
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Best Local Similarity 100.
Matches 129; Conservative
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P-PSDB; AAP95781.
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                                                                                                                                               JP01179687-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAATC 120
                                                                                                                                        virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced; infinenza; Ebola; Marburg; Arbovirus; hepatitis; respiratory syncytial virus; herpes simplex virus; human papilloma virus; HIV infection; ds; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enhancing the immunity of a host to infection of a first and second pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or HIV infections comprises administering to the host a first and a second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TIATICALAATGALAGIAGGAGGCTIGGIAGGITIAAGAATAGITTTIGCIGTACTITCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; SEQ ID NO 36; 185pp; English.
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                                                                                                                                                                                                                                                  Human immunodeficiency virus.
                                                                                                HIV p17/24 membrane form DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US018238
                                                                                                                                                                                                                                                                                                                                                                           17-MAR-2003; 2003US-00286332
                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-00585599
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                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant adenovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-851718/
P-PSDB; ADD66290.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WANG/) WANG D.
                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUN-2000;
                                                        15-JAN-2004
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24-0CT-2002

(revised)
(first entry)

25-MAR-2003 22-AUG-1990

AAN90531;

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Query Match Best Local S

Matches

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This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antiparasitic, protozoacide, cytostatic and antibacterial, antiparasitic, protozoacide, cytostatic and munomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Boola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malariar. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain, BHIO antigen construct described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced; influenza; Ebola; Marburg; Arbovirus; hepatitis; respiratory syncytial virus; herpes simplex virus; human papilloma virus; HIV infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2056 TTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCT
                                                                                                                                                                                                                  New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 129; DB 9; 100.0%; Pred. No. 2.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV clone BH10 Env_mdeltaCdeltaT_300 DNA.
                                                                                                                                                                                                                                                                                                            Claim 12; Fig 40; 156pp; English
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                                                 02-JUN-2000; 2000US-00585599.
                   01-NOV-2001; 2001US-00003035
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                                                                                                       (WANG/) WANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence is used in the exemplification of the invention.
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100.0%; Score 129; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.2e-30;
Matches 129; Conservative 0; Mismatches 0;
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                                                                                                                 2000US-00585599.
2001WO-US018238.
2001US-00003035.
                                                          17-MAR-2003; 2003US-00286332
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04-JUN-2001;
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31-AUG-1987;
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(REPK) REPLIGEN CORP

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                                                                                                                                                                           The sequence is the result of cloning a hybrid envelope gene from HIV variants BH10 and RF. A central portion of the RF gene was used, the rest being from te distantly related variant BH10. The resulting clone, pAcHT6 produces a hybrid gp 160 envelope protein with novel immunological and antigenic characteristics. It may be used to as a vaccine and for diagnosis and therapy of AIDS. See also AAN80948. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
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                                                                                                     Prodn. of recombinant HIV envelope proteins in insect cells - useful vaccine against AIDS and for diagnosis and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor
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                              Putney S, Jellis CL;
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Pred. No. 2.2e-30;
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                                                                                                                                                  Disclosure; Page ?; 4pp; English
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                            Carson H,
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Matches 129; Conservative
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                                                      WPI; 1988-176944/26.
P-PSDB; AAP80967.
                           Rusche J, Lynn D,
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                                                                                                     dequence encoding an HVV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the recombinant adenovirus elicits an immune response directed against the HVV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparasitic, protozoacide, cytostatic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic aminomodulatory activity. Bola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-strain BH10 antigen construct described in the disclosure of the
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                                                                                      invention describes a novel recombinant adenovirus comprising an HIV
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Pred. No. 2.2e-30;
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                                           Claim 12; Fig 47; 156pp; English
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Sequence 1, 1 Sequence 15, Sequence 15, Sequence 13, Sequence 13,

Sequence 3 Sequence 3 Sequence 9

Sequence Sequence Sequence 7

sequence 8, Sequence 8,

Sequence Sequence

us-10-003-035-74.rni

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1 ATGAGAGTGAAGAAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14. Application US/08029402
Patent No. 551657
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Murphy, Cheryl I.
APPLICANT: Young, Elihu
TITLE OF INVENTION: Baculovirus Vectors For Expression of
TITLE OF INVENTION: Secretory and Membrane-Bound Proteins
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMER: US/08/029,402
FILING DATE: 19930305
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/COCKET NUMBER: 30,353
REFERENCE/COCKET NUMBER: 30,353
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REFERENCE/COCKET NUMBER: 30,353
TELEPHONE: (202) 83-8716
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
"WUDE: NUTCHIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%; Score 90; DB 1; 1
1 Similarity 100.0%; Pred. No. 2.2e-21;
90; Conservative 0; Mismatches 0;
                                  US-08-488-5518-1
US-09-309-572-15
US-09-318-108-13
US-08-935-312-13
US-08-948-760B-33
US-08-646-538-35
US-08-648-312-35
US-08-648-318-35
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US-08-815-809-6
US-08-815-809-6
US-08-815-809-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Sterne, Kessler, Goldstein & Fox 1225 Connecticut Avenue
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JS-09-079-587-6
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TYPE: NUCLEIC ACID
STRANDEDNESS: both
                                                      9709
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COUNTRY: U.S.A.
ZIP: 20036
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Matches 90; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
US-08-029-402-14
                                                        Query Match
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Sequence 135, App
Sequence 138, App
Sequence 138, App
Sequence 141, App
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Sequence 1, Appli
Sequence 1, Appli
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Patent No. 5462872
Sequence 2, Appli
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1099.812 Million cell updates/sec
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Sequence 78,
                                                                                                                    March 11, 2004, 20:30:23 ; Search time 45.4128 Seconds
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Sequence 1
Sequence 9
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-417-210A-135
US-08-117-210A-138
US-08-117-210A-138
US-09-136-159A-138
US-09-136-159A-141
US-09-136-159A-141
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5-09-136-159A-78
5-09-124-900-1
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Maximum Match 100%
Listing first 45 summaries
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0; Gaps

Length 105

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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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10 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGGAGATGGGGCACCATG 69
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Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 90; Conservative 0; Mismatches 0; Indels
                                                                                                                                  Sequence 135, Application US/09136159A
Patent No. 6596279
GENERAL INFORMATION:
APPLICANT: Virgometics Corporation
APPLICANT: Partaglia, James
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I
TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
FILE REFERENCE: 454310-2690.1
CURRENT APPLICATION NUMBER: US/09/136,159A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/417,210A FILING DATE: 05-APR-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                  SSEE: CURTIS, MORRIS & SAFFORD, P.C.
1: 530 FIFTH AVENUE
NEW YORK
X: NEW YORK
XY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCTTGGGATGTTGATGATCTGTAGTGCT 386
                                                         CICCITGGGATGTTGATCTGTAGTGCT 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 2020 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                  STATE: NEW YORK
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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TYPE: nucleic acid
STRANDEDNESS: sing
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MOLECULE TYPE:
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US-09-136-159A-135
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CITY: N
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; OTHER INFORMATION: DNA sequence of the H6-promoted HIV1 gp120 + TM (with ELDKWA ep: , OTHER INFORMATION: opes) gene between C5 flanking arms, coding strand US-09-136-159A-135
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MEDIUM TYPE: RIODAY disk
COMPUTER: Bloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
ATTORNEY/ABENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELEOCOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 90; DB 4; L. Best Local Similarity 100.0%; Pred. No. 5.4e-21; Matches 90; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 1995-04-05
PRIOR APPLICATION NUMBER: US 08/223,842
PRIOR PILING DATE: 1995-04-06
PRIOR FILING DATE: 1992-04-06
PRIOR FILING DATE: 1992-06-11
PRIOR FILING DATE: 1992-06-11
PRIOR FILING DATE: 1991-06-14
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PRIOR FILING DATE: 1993-08-12
PRIOR FILING DATE: 1993-08-12
PRIOR PILING DATE: 1991-03-06
PRIOR PILING DATE: 1991-03-06
PRIOR PILING DATE: 1991-03-07
PRIOR FILING DATE: 1991-03-07
PRIOR FILING DATE: 1991-03-07
PRIOR FILING DATE: 1991-03-07
NUMBER OF SEQ ID NOS: 149
SEQ ID NO 135
LENGTH: 2020
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; Sequence 138, Application US/08417210A
; Patent No. 5863542
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ADDRESS:
ASSOCIATE, MORLIS &
ASSOCIATE AVENUE
T: NEW YORK
Y: USA
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APPLICANT: PROJECTI, ENZO
APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
TITLE OF INVENTION: IMMUNOBE?
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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297 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2060;
                                                                                                                   Sequence 141, 4pplication US/08417210A
Patent No. 5863542
GREERAL INFORMATION:
APPLICANT: PROLETTI, ENZO
APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
TITLE OF INVENTION: IMMUNOBERICIENCY RECOMBINANT POXVIRUS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSORESCE:
ADDRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 141. Application US/09136159A

Patent No. 6596279

GENERAL INFORMATION:
APPLICANT: Virogenetics Corporation
APPLICANT: Tartaglia, James
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I
FILE OF INVENTION: Immunodeficiency recombinant poxvirus
FILE OF INVENTION: Immunodeficiency recombinant
FILE OF INVENTION: Immunodeficiency recombinant
FILE OF INVENTION: 1890-08-14
FILE OF PRICATION NUMBER: US/09/136,159A
CURRENT FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-04-05
PRIOR FILING DATE: 1994-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: P-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.4e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C. STREET: 530 FIFTH AVENUE CITY: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 crechregearchicarcarchichacher
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100.0%; Pred. No. 5.4
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: KOWALEXT, THOWAS J.
REGISTRATION NUMBER: 32,147
REFRENCE/DOCKET NUMBER: 4543
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2060 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.(
Matches 90; Conservative
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                                                                                                         US-08-417-210A-141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGGTGGAGATGGGGCACCATG
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Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 90; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     Length 2028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 138, Application US/09136159A

Sequence 138, Application US/09136159A

GENERAL INFORMATION:
APPLICANT: Pacleti, Enzo
APPLICANT: Partaglia, James
APPLICANT: Partaglia, James
APPLICANT: Partaglia, James
APPLICANT: Tartaglia, James
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I

TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
FILE REFERENCE: 454310-2690.1
FILE REFERENCE: 454310-2690.1
FILE REPERENCE: 454310-2690.1
FRIOR FILING DATE: 1995-04-05
FRIOR FILING DATE: 1995-04-05
FRIOR FILING DATE: 1995-06-11
FRIOR APPLICATION NUMBER: US 07/715,921
FRIOR FILING DATE: 1991-06-14
FRIOR FILING DATE: 1991-03-07
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 90; DB 2; I
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 90; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 CTCCTTGGGATGTTGATGATCTGTAGTGCT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 Crccrreddardridardarcreracier 386
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INFORMATION FOR SEQ ID NO: 138: SEQUENCE CHARACTERISTICS: LENGTH: 2028 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin version 3.1
SEQ ID NO 138
LENGTH: 2028
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                                                                                                                                                                          linear
                                                                                                                                                                ; TOPOLOGY: li;
; MOLECULE TYPE:
US-08-417-210A-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-136-159A-138
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US-09-136-159A-138
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1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 60
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Patent No. 5714316

APLICANT: Weiner, David

APPLICANT: Weiner, David

APPLICANT: Weiner, David

APPLICANT: Weiner, David

TITLE OF INVENTION: Targeting

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P.O. Box 457

CITY: Spring House

STATE: Pennsylvania

COTHERS PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e-21;
Matches 90; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 15337.1534
OTHER INFORMATION: /note= ""gp120/gp41 cleavage site""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1 - OTHER INFORMATION: /note= "pre-HIV gpl60" US-07-916-098A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CICCIIGGGAIGIIGAIGAICIGIAGIGCI 90
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           NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELEPHONE: (312) 715-1000
TELEPHONE: (312) 715-1000
TELEFAX: 910/221-5317
TELERAX: 910/221-5317
TELERAX: 910/221-5317
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 LENGTH: 2571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
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88..2568
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRATURE:
NAME/KEY: SIG_PEPT
LOCATION: 1.87
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: H6-promoted HIV1 gp120 + TM (with ELDKWA epitopes) gene between A
; OTHER INFORMATION: 24R and K1L flanking arms, coding sequence
US-09-136-159A-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/07916098A

Patent No. 5871732

Patent No. 5871732

APPLICANT: BURKLY, LINDA C.

APPLICANT: CHISHOLM, PATRICIA L.

APPLICANT: THOMAS, DAVID W.

APPLICANT: ROSA, MARGARET D.

APPLICANT: ROSA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 60
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100.0%; Score 90; DB 4; L
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 90; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA.
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFFICATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: NO. 5871732ember 27, 1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 CTCCTTGGGATGTTGATGATCTGTAGTGCT 386
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PRIOR APPLICATION NUMBER: US 07/897,382
PRIOR FILING DATE: 1992-06-11
PRIOR FILING DATE: 1992-06-14
PRIOR PILING DATE: 1991-06-14
PRIOR PILING DATE: 1991-06-14
PRIOR PILING DATE: 1993-08-12
PRIOR PILING DATE: 1993-08-12
PRIOR PILING DATE: 1993-08-12
PRIOR FILING DATE: 1992-03-06
PRIOR FILING DATE: 1991-03-07
PRIOR FILING DATE: 1991-06-11
PRIOR PILING DATE: 1991-06-11
PRIOR PILING DATE: 1991-06-11
PRIOR APPLICATION NUMBER: US 07/666,056
PRIOR PILING DATE: 1991-03-07
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PATENT DATE: 1991-03-07
NUMBER OF SEQ ID NOS: 149
SEQ ID NO 141
LENGTH: 2060
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CITY: CHICAGO
STATE: 1LLINOIS
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION NUMBER: US/07/916,098A
FILING DATE: Unly 24, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-07-916-098A-1
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Patent No. 6492104

GENERAL INFORMATION:
APPLICANT: CLOYD, MILES W.
APPLICANT: CLOYD, MILES W.
TITLE OF INVENTION: BIA TEST USING NONDENATURED HIV ANTIGEN FOR EARLY
TITLE OF INVENTION: DETECTION OF HIV INFECTION
TITLE OF INVENTION: DETECTION OF HIV INFECTION
CURRENT APPLICATION NUMBER: US/09/325,131B
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 08/728,122
PRIOR APPLICATION NUMBER: 08/143,168
PRIOR FILING DATE: 1996-10-26
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGGTGGAGATGGGGCACCATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440 Argadangaangaanararcaccacritergagarargagagargagaragagacaccarg 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 2694;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 90; DB 1; Length 26; Best Local Similarity 100.0%; Pred. No. 5.9e-21; Matches 90; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 CTCCTTGGGATGTTGATGATCTGTAGTGCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500 crccirccarcircarcarcicracic 529
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRINCATION NUMBER: US 07/718,537
FILING DATE: 21-UW-1991
ATTORNEY/AGENT INFORMATION:
NAME: BAR, MARY E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST15AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEPHONE: 215-540-9200
TELEPRAX: 215-540-9200
TELEPRAX: 215-540-9200
TELEPRAX: 2694 base pairs
TYPE: mucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown;
MOLECULE TYPE: DNA (genomic)
US-08-147-890-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 90; Conserv
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US-09-325-131B-1
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RESULT 11 US-08-728-122-1

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470 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parent No. 1, Teprated Congress Avenue, Suite 1900

STARET: STARE STARES

APPLICANT: Cloyd, Miles W.

APPLICANT: Ramsey, Keith M.

TITLE OF INVENTION: A New EIA Test Using No. 6074646-Denatured TITLE OF INVENTION: HIV Antigen for Early Detection of TITLE OF INVENTION: HIV Infection NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.

STREET: 816 Congress Avenue, Suite 1900

CITY: Austin STREET: 1 Exas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2730;
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                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elab PC compatible
COMPUTER: Elab PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,122
FILING DATE: 09-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: 43424.0003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               530 CTCCTTGGGATGTTGATGATCTGTAGTGCT 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 90; DB
Best Local Similarity 100.0%; Pred. No. 5.9
Matches 90; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CTCCTTGGGATGTTGATGTCTGTAGTGCT 90
Sequence 1, Application US/08728122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (512) 499-6290 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2730 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                              STATE: Texas
COUNTRY: USA
ZIP: 78701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , LENGTH: 2945
5462872-1
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US-08-463-210-6

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                                                                                                                                                                        268 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATG 327
                                                                                                                 1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGGGAGATGGGGGCACCATG 60
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Sequence 2, Application US/08147890

Patent No. 5714316

GENERAL IMPORMATION:
APPLICANT: Weiner, David
APPLICANT: Williams, William
APPLICANT: Levy, David N.
ITILE OF INVENTION: Chimeric Envelope Proteins for Viral
ITILE OF INVENTION: Targeting
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: 20
CORRESPONDENCE ADDRESS: 3

CORRESPONDENCE ADDRESSE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457

CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 90; DB 1; Length 3084; 100.0%; Pred. No. 6.1e-21; ive 0; Mismatches 0; Indels (
Query Match
100.0%; Score 90; DB 6; Length 2945;
Best Local Similarity 100.0%; Pred, No. 6e-21;
Matches 90; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,890
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/718,537
FILING DATE: 21-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WETISAUSA
TELEPAX: 215-540-9200
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                                                                                                                                                                                                                                                                                      328 crecrreddardrigardarcreradiecr 357
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                                                                                                                                                                                                                                     90
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Best Local Similarity
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RESULT 14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09
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/note= "Corresponds to nucleotide positions 5580
to 9154 in figure 3 of US 06/693,866"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGGTGGAGATGGGGCACCATG
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Sequence 6, Application US/08463210
| Sequence 6, Application US/08463210
| Patent No. 6001977
| GENERAL INFORMATION:
| APPLICANT: CHANG, Nancy T. APPLICANT: WONG-STAAL, Flossie
| TILLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA NUMBER OF SEQUENCES: 11
| CORRESPONDENCE ADDRESS: 11
| CORRESPONDENCE ADDRESS: 11
| CORRESPONDENCE ADDRESS: 12
| STREET: 345 Park Avenue
| CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                           STATE: New TOLA

CONDTRY: USA

ZIP: 10154-0053

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER TRADABLE FORM:
MEDIUM TYPE: TONDS/MS-DOS
SOFTWARE: IBM PC COMPATIBLE
COMPUTER: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/463,210
FILING DATE: 05-UN-1995
CLASSIFICATION NUMBER: US 06/693,866
FILING DATE: 23-DAN-1985
FILING DATE: 23-DAN-1985
FILING DATE: 23-DAN-1985
FILING DATE: 10-OCT-1984
ATTORNEY/AGENT: INFORMATION:
APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-OCT-1984
ATTORNEY/AGENT INFORMATION:
NAME: SETUNIAN, LEBILE A.
REPERBENCE/COCKET NUMBER: 35,353
REPERBENCE/COCKET NUMBER: 35,353
REPERBENCE/COCKET NUMBER: 35,353
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 6:
SEGURACE CHARACTERISTICS:
TENCTH: 3563 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 90; DB 3; I Pred. No. 6.4e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CTCCTTGGGATGTTGATGATCTGTAGTGCT 90
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US-08-463-028-6
; Sequence 6, Application US/08463028
; Patent No. 6610476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
COCATION: 1.3563
COTHER INFORMATION: /notes:
COTHER INFORMATION: /notes:
COTHER INFORMATION: to 911
US-08-463-210-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3563 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HTLV-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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Search completed: March 11, 2004, 23:12:15 Job time : 47.4128 secs OGVGU63TV ZMMBBC002 ZUAFN74TH ik30c12.9 CH230-591

ZUAFM74TH OGWBT24TV ZUAHN35TV ph18c07.y ph3ac09.y ph3ac09.y ph89h12.y

EST423618 EST423322 BMBAC317B EST537828 EST623842 EST707702 EST536012 EST536013 EST623843

EST709520 pz08f12.y zuabe85TH

OGWHN17TH ZMMBBb017

OGULX43TV OGUKC77TH ZUABX13TH

BJ368213

BJ366287 BJ397521 BJ368768

BJ370269 BJ370029

BJ425039 BJ424063 BJ367814 BJ425027

Fri

Title: Perfect score:

Sequence:

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on:

Run ĕ

Scoring table:

Searched:

Database

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus. 1 (bases 1 to 145)
Wang, Y.L., Saigoh, K., Osaka, H., Yamanishi, T., Suh, J.G.,
Kiyosawa, H., Sakai, Y., Wakana, S. and Wada, K.
YAC/BAC-Based physical and transcript mapping around the gracile axonal dystrophy (gad) locus identifies uchli, pmx2b, atp3a2, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Keiji Wada
Department of Degenerative Neurological Diseases
National Institute of Neuroscience, NCNP
4-1-1, Ogawahigashi, Kodaira, Tokyo 187-8502, Japan
Email: wada@ncnp.go.jp
RT-FCR primer based on the sequence that isolated from mouse BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB036493 Mus musculus CJ7 brain, liver, kidney, lung, heart Mus
musculus cDNA clone 15-5, mRNA sequence.
CG453685
CG416525
CG61624834
CC167485
CG676625
CC676625
CC676625
CC676625
CC676625
CC676625
CC676625
CC676625
CC676625
BD699257
BD699953
BD699953
BD699953
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BD699953
BD6999953
BD6999953
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BD6999953
CC676599
CC676289
CC67659
BD699995
CC676999
BD79699
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CG455885
CG19444
CG118448
CG167485
CC167485
CC167485
CC676640
CC670625
CC67
                                                                                                                                                                                                                                                                     B1433251
B0516428
CK263442
CK263442
CK263442
CG292820
CG29221
CC731389
CC667508
BJ411212
BJ370029
BJ36029
BJ36029
BJ36029
BJ3629
BJ3629
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BJ3629
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BJ3629
BJ3629
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                                                                                                                                                                                                                           B1435067
BQ516427
CK261624
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Mus musculus
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AB036493.1 GI:6854226
 genea
10873389
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 LOCUS
DEFINITION
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ORGANISM
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
MEDLINE
PUBMED
COMMENT
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AUTHORS
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AB036493
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 X88515 H. sapiene D
CG788669 ZMMBBb024
CG453676 OGVGU63TH
                                                                                              March 11, 2004, 19:37:35; Search time 2481.77 Seconds (without alignments) 1552.207 Million cell updates/sec
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                                                                                                                                                                                   1 ttattcataatgatagtagg.....acctcccaatcccgagggga 129
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             5.1.6
Compugen Ltd.
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             GenCore version
Copyright (c) 1993 - 2004
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CG788669
CG453676
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Maximum Match 100%
Listing first 45 summaries
                                                                      nucleic search, using sw model
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em_esthum.*
em_estov...*
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gb_estl..*
gb_estl..*
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em_estpl..*
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em_gss_hum..*
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em_gss_ppg;
em_gss_vrl:
gb_gssl:*
gb_gss2:*
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Maximum DB seq length: 200000000
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816
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54.3
29.0
27.8
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Pred. No.

score ga

79 70 37.4 35.8

Score

No. Result

EST 22-AUG-2000

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CG788669 110 bp DNA linear GSS 07-NOV-2003
ZMMBBb0243B19.r ZMMBBb Zea mays subsp. mays genomic clone
ZMMBBb0243B19 3', genomic survey sequence.
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5
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta; Embryophyta;

Ragnoliophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae, Andropogoneae; Zea.

1 (Dasea 1 to 110)

1 (Dasea 1 to 110)

Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.

and Wing, R.
                                                        8 iiaaiaaaaindiiidaidaitiiindeliaaaaaaaaaiiiiaaGdaiiiaaadia 67
                                 59
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                                 1 TTATTCATAATGATAGTAGGAGGCTTGGTAGGT-TTAAGAATAGTTTTTGCTGTACTTTC
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="ZNMBBb"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing of the maize genome Unpublished (2003)
Contact: Rod Wing Arizona Institute
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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Indels
 13;
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Pred. No. 0.84;
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 0; Mismatches
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Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR PRIMERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/cultivar="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMMBBb0243B19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTAAAAGTGTTAGTTATGGATTTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
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Seq primer: M13r
Class: BAC ends.
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 Conservative
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Best Local Simi
Matches 56;
   95;
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CG453676
LOCUS
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CG788669
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                                                                                                                                                                                                                                                                                                                                                                                                 -----TAAGAATAGITTTTGCTG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                 33 riaricaraargaragraggaggcriggraggrigraagraaracargraarfrirgcrg 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen.H., Chrast,R., Rossier,C., Morris,M.A., Lalioti,M.D. and Antonarakis,S.E.
Cloning of 559 potential exons of genes of human chromosome 21 by
                                                                                                                                                                                   /tissue_type="brain, liver,kidney,lung,heart"
/cell_line="CJ7 embryonic stem cell line"
/dev_stage="adult"
/clone_lib="Mus musculus CJ7 brain, liver, kidney, lung,
heart"
                                                                                                                                                                                                                                                                                                                                                              Gaps
     clones (414D20,220F19, Research Genetics) using exon trapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSMC01D05 232 bp DNA linear GSS 29-M
H.sapiens DNA for trapped exon (ID HMC01D05), genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 TACTITCIGIAGIGAATAGAGITAGGCAGGGATAITCACCAITAICGIITCAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 TACTITCIGIAGIGAATAGAGTIAGGCAGGGATAITCACCAITAICGTITCAG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 232)
Chen, H.M., Rossier, C., Chrast, R. and Antonarakis, S.E.
Cloning of trapped exons from human chromosome 21
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70; DB 29; Length 232; Pred. No. 1.7e-10;
                                                                                                                                                                                                                                                                                                                       61.2%; Score 79; DB 9; Length 145; ilarity 88.5%; Pred. No. 3.2e-13; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 1 TTATICATAATGATAGTAGGAGGCTIGGTAGGTT
                                                        1. .145
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129/Sv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon trapping
Genome Res. 6 (8), 747-760 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="21"
                                                                                                                           'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .232
/note="trapped exon"
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                                     Location/Qualifiers
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                                                                                                                                                               clone="15-5"
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X88515.1 GI:1437515
                                                                                                                                                                                 sex="male"
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Antonarakis, S.E.
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Best Local Similarity
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/db_xref="taxon:4577"
/clone="zwBwa0479K05"
/clone_lib="ZM_0.7 l.5_KB"
/note="Wetcor: pBGSK-; Site_1: HinclI; 0.7-1.5 kb
methylation filtered genomic_DNA library"
                                                                                                                                                        /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                    organism="Zea mays"
                                                          Seg primer: TF
Class: sheared ends.
Location/Qualifiers
  Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG416525.1 GI:34561370
                                                                                                                                                                                                                                                                                                                               ch 27.8%;
1 Similarity 63.2%;
55; Conservative
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Matches 55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525 TTAATAAAATAGTGGTATGATTTTTAGGTTAAATAAGGATTTTTAAGGCATTTTAAGTA 584
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                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                      1 (bases 1 to 816)
Mitchaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSS: OGVGU63TV
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 851)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budinan, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TICATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCTGTA
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OGVGU63TH ZM_0 7_1.5_KB Zea mays genomic clone ZMMBMa0479K05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /moi_type="genomic DNA"

| Agrain="BT3"
| Ab xxef="taxon:4577"

| /clone="ZMMBMa0479K05"

| /clone="ZMMBMa0479K05"

| /clone="ZMW 07" 1.5 KB"

| /note="Woctor" BBGSK-; Site 1: HincII; 0.7-1.5 Kb

methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                               TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
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/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
                    genomic survey sequence.
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                                                      CG453676.1 GI:34838676
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                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301-838-5843
Fax: 301-838-0208
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1 (bases 1 to 936)

Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C., Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.
Sequencing of the maize genome at PGIR (2003c)
Unpublished (2003)

Outlact: Bharti, A.K.

Dr. Joachim Messing's lab

The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                  705 TTAATAAAATAGTGGTATGATTTTAGGTTAAATAAGGATTTTTAAGGA 646
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/clone lib="ZMMBBC (EcoRI)".
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
                                                                                                                                                                                                                                                                                                                                                                               CG416525
ZMMBBC0024C16f ZMMBBC (ECORI) Zea mays subsp. mays genomic clone
                                                                                                     4 TICATAAIGATAGTAGGAGGCTIGGIAGGITITAAGAAIAGITTTIGCIGIACTITICIGIA
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     Length
                                                  Indels
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Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
     29;
                                                  32;
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/mol type="genomic DNA"
/cultivar="B73"
     BB
Score 35.8; Di
Pred. No. 3.3;
0; Mismatches
                                                                                                                                                                                                                                                  645 GirraakGrariaGrrcrGGArrira 619
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Location/Qualifiers
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/db_xref="taxon:4578"
/clone="ZMMBBc0024C16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays subsp. mays (maize)
Zea mays subsp. mays
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/clone lib="WGGs-ZmaygF (DH5a methyl filtered)"
/note="Corgan: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nuclecitie was
added by fill in in the recessive 3' end. The genomic DNA
was nabulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
fractionated using sephadex and were cloned into the vector (:x/y
reads in Milamply, .b/g reads in pUCl9). The same ligation
was transformed into DH5a."
                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                              Rabinowicz, P. D. (%2, Klug, L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Miller, S., Nascimento, L., Zutavern, T., McCombie, W. R. and Martienseen, R. A. Gutavern, T., McCombie, W. R. and Martienseen, R. A. Genomic shotgun sequences from Zea mays (methyl-filtered) Unpublished (2002)

L. Onteac: W. R. Achard McCombie

Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8874

Email: mcCombie@cshl.org
Plate: ik30 row. c column: 12
Seq primer: -1M13UnivRev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ik30c12"
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Location/Qualifiers
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/organism="Zea mays"
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Best Local Similarity
Matches 54; Conserv
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/clone="xmMBPa0052N04"
/clone llb="Xm_3.04.0 KB"
/note="Vector: pBCSK"; Site_1: HincII; 3-4 kb 'unfiltered'
genomic DNA library"
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Whitelaw (C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw (C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSS: ZUAFN/ATV
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Tel: 301-838-5843
Fax: 301-838-0208
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    Pred. No. 3.4;
0; Mismatches
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/mol_type="genomic DNA"
/strain="B73"
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Location/Qualifiers
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    63.2%;
                          55; Conservative
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BH332797 174 CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-5917, genomic survey sequence.
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                                                                                                                                                                     540 itaataaaatagiggrafgattittaggitaaaraaggaattitaagggattiaagta 599
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Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Zhao, S., Shetty, J., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
                                                                                                                       63
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                    TICATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCTGTA
                                                             ;
0
      Length 782;
                                                                Indels
26.5%; Score 34.2; DB 28; 62.1%; Pred. No. 9.9; iive 0; Mismatches 33;
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63

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OGWBT24TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0531C24, genomic survey sequence.
                                                       660 TIAATAAAAATIGGTTTTTAGGTTAAATAATAAGGGATTTTAAGGTATTTAAAGTA 719
                                                                                                                                                                                                                                                                                                                                                          248 TTAATAAAAATAGTTTTGTGATTTTTAGGTTAAATAAGGAATTTTTAAGGCATTTTAAGTA 189
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                       4 TTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCTGTA
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/clone lib="xxm 0.7 1.5 KB"
methylation filtered genomic DNA library"
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Pred. No. 10;
0; Mismatches 33;
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Class: sheared ends.
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l Similarity 62.1%;
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ZUARM74TH ZM 3.0 4.0 KB Zea mays genomic clone ZMMBPa0052N03,
CC986340
CC986340.1 GI:33846216
                                                                                                                                  Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, plase contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 59 row: I column: 7
Seq primer: SP6
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Cotsortium for Maize Genomics
Uppublished (2002)
Cottages ZIARMATV
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Contages ZIARMATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Brain"
/clone_lib="CHORI-210 Segment 1" :
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoR
CHORI-230 Rat (BN/SENHsd/MCW) BAC library produced by
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                                                                              USA
                                                                              MD 20850,
                                                                                                                                                                                                                                                                                                                                                                               organism="Rattus norvegicus"
                Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MI
Tel: 301 838 0200
Tel: 301 838 0200
Email: szhao@eigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.5%; Score 34.2; 3 62.1%; Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
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/db_xref="taxon:10116"
/clone="CH230-5917"
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1. .794
  GSSs: CH230-5917.TV
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Seg primer: TR
Class: sheared ends.
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54; Conservative
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Fax: 301-838-0208
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Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R., Jackson,Y., Cardenas,M., The Washington Univ. Nematode EST Project, 1999

AL Unpublished (1999)
Contact: McCarter JP
The Mashington Univ. Nematode EST Project, 1999
Washington Univ. Nematode EST Project, 1999
The Mashington Univ. Nematode EST Project, 1999
Fax: 314 286 1810
Fax: 4 Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center
High quality sequence stop: 418.

1 Location/Qualifiers
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/clone_lib="Gotertagia ostertagi L3 pAMP1 v1"
/note="Vector: pAMP1 (Gibco); Site_1: Not1; Site_2: SalI;
***MARNING: Subsequent examination of these samples has
revealed the presence of an additional Tichostrongyloidea
cattle nematode, Cooperia oncophora. Sequences in this
library may derive from either Ostertagia or Cooperia.**

The library was constructed by Claire Murphy and Dr. James
McCarter at Washington University, St. Louis. The CDNA was
made by using Dynabaad oligo-dT priming (Dynal). PCR based
library using a modified protocol from the SWART PCR CDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of pAMP1. Nematodes were provided by Dr. Louis
Gasbarree of the USDA, Beltsville, MD
(lgasbarreanri.barc.usda.gov). Third stage exsheathed
larvae were collected from 14 day fecal-sphagnum moss
cultures of Ostertagia eggs. The larvae were recovered by
overnight passage through a 20 micron nylon mesh. The
larvae were then subjected to a treatment with 1.25¢
larvae were then subjected to a treatment which 1.25¢
changes of PBS and then pelleted and snap frozen in
liquid nitrogen."
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bA28405.y2 Ostertagia ostertagi L3 pAMP1 v1 Ostertagia ostertagi cDNA 5' similar to SW:GCH1 OSTOS 061573 GTP CYCLOHYDROLASE I contains Alu repetitive element;, mRNA sequence.
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llarity 62.7%; Pred. No. 16;
Conservative 0; Mismatches 31;
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/mol_type="mRNA" | foldoxer feet | foldoxer f
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Bukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.
1 (bases 1 to 513)
McCarter,J., Clifton;S., Chiapelli,B., Pape,D., Martin,J.,
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/clone="ZMMBPa0070F22"
/clone="Jbb="ZM_3.0_4.0_KB"
/note="Vector: pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered'
genomic DNA library"
                                                                                                                                                                                                                                                                                     CG464137 J. 2.0_4.0_KB Zea mays genomic clone ZMMBPa0070F22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae; PACCAD calde; Panicoideae; Andropogonee; Zea.

(Dases 1 to 935)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Rohlfing, T., Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
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ph18c07.y2 Ostertagia ostertagi L3 pAMP1 v1 Ostertagia ostertagi cDNA 5' similar to SW:GCH1 OSTOS 061573 GTP CYCLOHYDROLASE I contains Alu repetitive element;, mRNA sequence.
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Similarity 62.1%; Pred. No. 10;
54; Conservative 0; Mismatches
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/mol_type="genomic DNA"
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                                                                                                                    720 GİTTAAAĞCAİTAĞITCTĞĞAİTTİTA 746
                                                      64 GTGAATAGAGTTAGGCAGGGATATTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: whitelaw@tigr.org
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Other GSSS: ZUAHN35TH
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Class: sheared ends
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/dab="0etertagia ostertagia ostertagia or cotor: pAMP1 (dibco); Site 1: Not1; Site 2: Sal1;
/note="vector: pAMP1 (dibco); Site 1: Not1; Site 2: Sal1;
/evealed the presence of an additional Trichostrongyloidea revealed the presence of an additional Trichostrongyloidea cattle nematode, Cooperia oncophora. Sequences in this cattle nematode, Cooperia oncophora. Sequences in this The library may derive from either Ostertagia or Cooperia.***

The library may derive from either Ostertagia or Cooperia.***

McCarter at Washington University, St. Louis. The CDNA was made by using a modified protocol from the SMRAR PKR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Louis Gasbarree of the USDA, Beltsville, MD Gasbarree of the USDA, Beltsville, MD (lgasbarrean: barc.usda.gov). Third stage exsheathed larvae were collected from 14 day fecal-sphagnum moss cultures of Ostertagia eggs. The larvae were recovered by overnight passage on a Baermann apparatus, and then cleaned by passage through a 20 micron nylon mesh. The larvae were then subjected to a treatment with L258 and with
                                                                                                                                                                                                                                                                                                                                                                                 I (bases 1 to 536)

S McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Walter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Bucter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., McCann, R., Waterston, R. and Wilson, R., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Unpublished (1999)

L. Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington Univ. Nematode EST Project, 1999

Washington Univ. Nematode EST Project, 1999

Washington Univ. Nematode EST Project, 1999

Fax: 314 286 1800

Fax: 314 286 1810
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                                                                                                                                                                                                        Ostertagia ostertagi
Osterragia ostertagi
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.
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The library was constructed by Claire Murphy and Dr. James McCarter
at Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center
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contains Alu repetitive element;, mRNA sequence.
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ilarity 62.7%; Pred. No. 16;
Conservative 0; Mismatches 31;
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BQ099653.1 GI:20132637
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/clone libe="Ostertagia ostertagi L3 pAMPI v1"
/note="Vector: pAMPI (Gibco); Site_1: NotI; Site_2: SalI;
****MANING: Subbequent examination of these samples has
revealed the presence of an additional Trichostrongyloidea
cattle nematode, Cooperia oncophora. Sequences in this
library may derive from either Ostertagia or Cooperia.**
The library was constructed by Claire Murphy and Dr. James
McCarrer at Washington University, St. Louis. The CDNA was
made by using a modified protocol from the SMART PCR based
library using a modified protocol from the SMART PCR cDNA
library using a modified protocol from the SMART PCR CDNA
library using a modified brotocol from the SMART CR CDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of pAMPI. Nematodes were provided by Dr. Louis
Gasbarree of the USDA, Beltsville, MD
(lgasbaraanri.barc.usda.gov). Third stage exsheathed
larvae were collected from 14 day fecal sphagnum moss
cultures of Ostertagia eggs. The larvae were recovered by
overnight passage through a 20 micron nylon mesh. The
larvae were then subjected to a treatment with 1.25¢
cholor to induce excystation. The larvae were washed with
standary and then pelleted and snap frozen in
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The library was constructed by Claire Murphy and Dr. James McCarter
The library was constructed by Claire Murphy and Dr. James McCarter
The Mashington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center
High quality sequence stop: 419.

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Trichostrongyloidea, Haemonchidae, Ostertaglinae, Ostertagla.
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                                                                                                                              " (bases 1 to 535)
MCCarter, J. Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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llarity 62.7%; Pred. No. 16;
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